

SEQUENCE LISTING

<110> Glucksmann, Maria A.
Curtis, Rory A.J.
Tsai, Fong-Ying
Hodge, Martin R.
Meyers, Rachel E.
MacBeth, Kyle J.
Bandaru, Rajasekhar

<120> NOVEL 14275, 54420, 8797, 27439, 68730,
69112 AND 52908 MOLECULES AND USES THEREFOR

<130> MPI04-002OMNIM

<150> US 09/945,254
<151> 2001-08-31

<150> US 60/229,829
<151> 2000-08-31

<150> US 09/945,301
<151> 2001-08-31

<150> US 60/229,301
<151> 2000-09-01

<150> US 10/007,399
<151> 2001-11-05

<150> US 09/390,039
<151> 1999-09-03

<150> US 09/146,416
<151> 1998-09-03

<150> US 10/024,036
<151> 2001-12-17

<150> US 60/258,222
<151> 2000-12-22

<150> US 10/103,458
<151> 2002-03-22

<150> US 09/544,797
<151> 2000-04-07

<150> US 10/192,440
<151> 2002-07-10

<150> US 60/341,953
<151> 2001-12-19

<150> US 60/304,243
<151> 2001-07-10

<160> 62

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 1877
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (284)...(1438)

<400> 1
cgcgtccgct gagccctcac gggacatctg tgccctcat gggacacctg tgtcctcaca 60
gtacacttgt gacccttcca ggacacctta ctggtagaat tagtgtagct gccccaccc 120
tgaggccaag gacaccattg tctcaggaag gctgaagacc acaggctcct ggggggacag 180
agggcaggtg gggccctca ggaccctcct tggtggaaac caagaccagc aaggcgggtg 240
gctccacctt gcgtcgggcc tcagtcagcc cccgggggag gcc atg aac gcc acg 295
Met Asn Ala Thr
1
ggg acc ccg gtg gcc ccc gag tcc tgc caa cag ctg gcg gcc ggc ggg 343
Gly Thr Pro Val Ala Pro Glu Ser Cys Gln Gln Leu Ala Ala Gly Gly
5 10 15 20
cac agc cgg ctc att gtt ctg cac tac aac cac tcg ggc cgg ctg gcc 391
His Ser Arg Leu Ile Val Leu His Tyr Asn His Ser Gly Arg Leu Ala
25 30 35
ggg cgc ggg ggg ccg gag gat ggc ggc ctg ggg gcc ctg cgg ggg ctg 439
Gly Arg Gly Gly Pro Glu Asp Gly Gly Leu Gly Ala Leu Arg Gly Leu
40 45 50
tcg gtg gcc gcc agc tgc ctg gtg gtg ctg gag aac ttg ctg gtg ctg 487
Ser Val Ala Ala Ser Cys Leu Val Val Leu Glu Asn Leu Leu Val Leu
55 60 65
gcg gcc atc acc agc cac atg cgg tcg cga cgc tgg gtc tac tat tgc 535
Ala Ala Ile Thr Ser His Met Arg Ser Arg Arg Trp Val Tyr Tyr Cys
70 75 80
ctg gtg aac atc acg ctg agt gac ctg ctc acg ggc gcg gcc tac ctg 583
Leu Val Asn Ile Thr Leu Ser Asp Leu Leu Thr Gly Ala Ala Tyr Leu
85 90 95 100
gcc aac gtg ctg ctg tcg ggg gcc cgc acc ttc cgt ctg gcg ccc gcc 631
Ala Asn Val Leu Leu Ser Gly Ala Arg Thr Phe Arg Leu Ala Pro Ala
105 110 115
cag tgg ttc cta cgg gag ggc ctg ctc ttc acc gcc ctg gcc gcc tcc 679
Gln Trp Phe Leu Arg Glu Gly Leu Leu Phe Thr Ala Leu Ala Ala Ser
120 125 130
acc ttc agc ctg ctc ttc act gca ggg gag cgc ttt gcc acc atg gtg 727
Thr Phe Ser Leu Leu Phe Thr Ala Gly Glu Arg Phe Ala Thr Met Val
135 140 145
cgg ccg gtg gcc gag agc ggg gcc acc aag acc agc cgc gtc tac ggc 775
Arg Pro Val Ala Glu Ser Gly Ala Thr Lys Thr Ser Arg Val Tyr Gly
150 155 160
ttc atc ggc ctc tgc tgg ctg ctg gcc gcg ctg ctg ggg atg ctg cct 823

Phe	Ile	Gly	Leu	Cys	Trp	Leu	Leu	Ala	Ala	Leu	Leu	Gly	Met	Leu	Pro		
165					170					175					180		
ttg	ctg	ggc	tgg	aac	tgc	ctg	tgc	gcc	ttt	gac	cgc	tgc	tcc	agc	ctt	871	
Leu	Leu	Gly	Trp	Asn	Cys	Leu	Cys	Ala	Phe	Asp	Arg	Cys	Ser	Ser	Leu		
				185					190					195			
ctg	ccc	ctc	tac	tcc	aag	cgc	tac	atc	ctc	ttc	tgc	ctg	gtg	atc	ttc	919	
Leu	Pro	Leu	Tyr	Ser	Lys	Arg	Tyr	Ile	Leu	Phe	Cys	Leu	Val	Ile	Phe		
			200					205					210				
gcc	ggc	gtc	ctg	gcc	acc	atc	atg	ggc	ctc	tat	ggg	gcc	atc	ttc	cgc	967	
Ala	Gly	Val	Leu	Ala	Thr	Ile	Met	Gly	Leu	Tyr	Gly	Ala	Ile	Phe	Arg		
		215					220					225					
ctg	gtg	cag	gcc	agc	ggg	cag	aag	gcc	cca	cgc	cca	gcg	gcc	cgc	cgc	1015	
Leu	Val	Gln	Ala	Ser	Gly	Gln	Lys	Ala	Pro	Arg	Pro	Ala	Ala	Arg	Arg		
	230					235					240						
aag	gcc	cgc	cgc	ctg	ctg	aag	acg	gtg	ctg	atg	atc	ctg	ctg	gcc	ttc	1063	
Lys	Ala	Arg	Arg	Leu	Leu	Lys	Thr	Val	Leu	Met	Ile	Leu	Leu	Ala	Phe		
245					250					255					260		
ctg	gtg	tgc	tgg	ggc	cca	ctc	ttc	ggg	ctg	ctg	ctg	gcc	gac	gtc	ttt	1111	
Leu	Val	Cys	Trp	Gly	Pro	Leu	Phe	Gly	Leu	Leu	Leu	Ala	Asp	Val	Phe		
				265					270					275			
ggc	tcc	aac	ctc	tgg	ggc	cag	gag	tac	ctg	cgg	ggc	atg	gac	tgg	atc	1159	
Gly	Ser	Asn	Leu	Trp	Ala	Gln	Glu	Tyr	Leu	Arg	Gly	Met	Asp	Trp	Ile		
			280					285					290				
ctg	gcc	ctg	gcc	gtc	ctc	aac	tgc	gcg	gtc	aac	ccc	atc	atc	tac	tcc	1207	
Leu	Ala	Leu	Ala	Val	Leu	Asn	Ser	Ala	Val	Asn	Pro	Ile	Ile	Tyr	Ser		
		295					300					305					
ttc	cgc	agc	agg	gag	gtg	tgc	aga	gcc	gtg	ctc	agc	ttc	ctc	tgc	tgc	1255	
Phe	Arg	Ser	Arg	Glu	Val	Cys	Arg	Ala	Val	Leu	Ser	Phe	Leu	Cys	Cys		
	310					315					320						
ggg	tgt	ctc	cgg	ctg	ggc	atg	cga	ggg	ccc	ggg	gac	tgc	ctg	gcc	cgg	1303	
Gly	Cys	Leu	Arg	Leu	Gly	Met	Arg	Gly	Pro	Gly	Asp	Cys	Leu	Ala	Arg		
325					330					335					340		
gcc	gtc	gag	gct	cac	tcc	gga	gct	tcc	acc	acc	gac	agc	tct	ctg	agg	1351	
Ala	Val	Glu	Ala	His	Ser	Gly	Ala	Ser	Thr	Thr	Asp	Ser	Ser	Leu	Arg		
				345					350					355			
cca	agg	gac	agc	ttt	cgc	ggc	tcc	cgc	tgc	ctc	agc	ttt	cgg	atg	cgg	1399	
Pro	Arg	Asp	Ser	Phe	Arg	Gly	Ser	Arg	Ser	Leu	Ser	Phe	Arg	Met	Arg		
			360					365					370				
gag	ccc	ctg	tcc	agc	atc	tcc	agc	gtg	cgg	agc	atc	tga	agttgcagtc			1448	
Glu	Pro	Leu	Ser	Ser	Ile	Ser	Ser	Val	Arg	Ser	Ile	*					
		375					380										
ttgcgtgtgg	atggtgcagc	caccgggtgc	gtgccaggca	ggccctcctg	gggtacagga											1508	
agctgtgtgc	acgcagcctc	gcctgtatgg	ggagcaggga	acgggacagg	ccccatggt											1568	
cttcccggtg	gcctctcggg	gcttctgacg	ccaaatgggc	ttcccatggt	caccctggac											1628	
aaggaggcaa	ccacccacc	tccccgtagg	agcagagagc	accctggtgt	gggggcgagt											1688	
gggttcccca	caaccccgct	tctgtgtgat	tctggggaag	tcccggcccc	tctctgggcc											1748	
tcagtagggc	tcccaggctg	caaggggtgg	actgtgggat	gcattgcctg	gcaacattga											1808	

agttcgatca tggtaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1868
 aaaaaaaaaa 1877

<210> 2
 <211> 384
 <212> PRT
 <213> Homo sapiens

<400> 2
 Met Asn Ala Thr Gly Thr Pro Val Ala Pro Glu Ser Cys Gln Gln Leu
 1 5 10 15
 Ala Ala Gly Gly His Ser Arg Leu Ile Val Leu His Tyr Asn His Ser
 20 25 30
 Gly Arg Leu Ala Gly Arg Gly Gly Pro Glu Asp Gly Gly Leu Gly Ala
 35 40 45
 Leu Arg Gly Leu Ser Val Ala Ala Ser Cys Leu Val Val Leu Glu Asn
 50 55 60
 Leu Leu Val Leu Ala Ala Ile Thr Ser His Met Arg Ser Arg Arg Trp
 65 70 75 80
 Val Tyr Tyr Cys Leu Val Asn Ile Thr Leu Ser Asp Leu Leu Thr Gly
 85 90 95
 Ala Ala Tyr Leu Ala Asn Val Leu Leu Ser Gly Ala Arg Thr Phe Arg
 100 105 110
 Leu Ala Pro Ala Gln Trp Phe Leu Arg Glu Gly Leu Leu Phe Thr Ala
 115 120 125
 Leu Ala Ala Ser Thr Phe Ser Leu Leu Phe Thr Ala Gly Glu Arg Phe
 130 135 140
 Ala Thr Met Val Arg Pro Val Ala Glu Ser Gly Ala Thr Lys Thr Ser
 145 150 155 160
 Arg Val Tyr Gly Phe Ile Gly Leu Cys Trp Leu Leu Ala Ala Leu Leu
 165 170 175
 Gly Met Leu Pro Leu Leu Gly Trp Asn Cys Leu Cys Ala Phe Asp Arg
 180 185 190
 Cys Ser Ser Leu Leu Pro Leu Tyr Ser Lys Arg Tyr Ile Leu Phe Cys
 195 200 205
 Leu Val Ile Phe Ala Gly Val Leu Ala Thr Ile Met Gly Leu Tyr Gly
 210 215 220
 Ala Ile Phe Arg Leu Val Gln Ala Ser Gly Gln Lys Ala Pro Arg Pro
 225 230 235 240
 Ala Ala Arg Arg Lys Ala Arg Arg Leu Leu Lys Thr Val Leu Met Ile
 245 250 255
 Leu Leu Ala Phe Leu Val Cys Trp Gly Pro Leu Phe Gly Leu Leu Leu
 260 265 270
 Ala Asp Val Phe Gly Ser Asn Leu Trp Ala Gln Glu Tyr Leu Arg Gly
 275 280 285
 Met Asp Trp Ile Leu Ala Leu Ala Val Leu Asn Ser Ala Val Asn Pro
 290 295 300
 Ile Ile Tyr Ser Phe Arg Ser Arg Glu Val Cys Arg Ala Val Leu Ser
 305 310 315 320
 Phe Leu Cys Cys Gly Cys Leu Arg Leu Gly Met Arg Gly Pro Gly Asp
 325 330 335
 Cys Leu Ala Arg Ala Val Glu Ala His Ser Gly Ala Ser Thr Thr Asp
 340 345 350
 Ser Ser Leu Arg Pro Arg Asp Ser Phe Arg Gly Ser Arg Ser Leu Ser
 355 360 365
 Phe Arg Met Arg Glu Pro Leu Ser Ser Ile Ser Ser Val Arg Ser Ile
 370 375 380

<210> 3
 <211> 269

<223> Description of Unknown Organism: Transmembrane Receptor of the Rhodopsin Superfamily

<400> 3

Gly 1	Asn	Ile	Leu	Val 5	Ile	Trp	Val	Ile	Cys 10	Arg	Tyr	Arg	Arg	Met 15	Arg
Thr	Pro	Met	Asn 20	Tyr	Phe	Ile	Val	Asn 25	Leu	Ala	Val	Ala	Asp 30	Leu	Leu
Phe	Ser	Leu 35	Phe	Thr	Met	Pro	Phe 40	Trp	Met	Val	Tyr	Tyr 45	Val	Met	Gln
Gly	Arg 50	Trp	Pro	Phe	Gly	Asp 55	Phe	Met	Cys	Arg	Ile 60	Trp	Met	Tyr	Phe
Asp 65	Tyr	Met	Asn	Met	Tyr 70	Ala	Ser	Ile	Phe	Phe 75	Leu	Thr	Cys	Ile	Ser 80
Ile	Asp	Arg	Tyr	Leu 85	Trp	Ala	Ile	Cys	His 90	Pro	Met	Arg	Tyr	Met 95	Arg
Trp	Met	Thr	Pro	Arg 100	His	Arg	Ala	Trp 105	Val	Met	Ile	Ile	Ile 110	Ile	Trp
Val	Met	Ser 115	Phe	Leu	Ile	Ser	Met 120	Pro	Pro	Phe	Leu	Met 125	Phe	Arg	Trp
Ser	Thr 130	Arg	Tyr	Asp	Glu	Asn 135	Glu	Trp	Asn	Met	Thr 140	Trp	Cys	Met	Ile
Tyr 145	Asp	Trp	Pro	Glu	Trp 150	Met	Trp	Arg	Trp	Tyr 155	Val	Ile	Leu	Met	Thr 160
Ile	Ile	Met	Gly	Phe 165	Tyr	Ile	Pro	Met	Ile 170	Ile	Met	Leu	Phe	Cys 175	Tyr
Trp	Arg	Ile	Tyr 180	Arg	Ile	Ala	Arg	Leu 185	Trp	Met	Arg	Met	Ile 190	Pro	Ser
Trp	Gln 195	Arg	Arg	Arg	Arg	Met	Ser 200	Met	Arg	Arg	Glu	Arg 205	Arg	Ile	Val
Lys	Met 210	Leu	Ile	Ile	Ile	Met 215	Val	Val	Phe	Ile	Ile 220	Cys	Trp	Leu	Pro
Tyr 225	Phe	Ile	Val	Met	Phe 230	Met	Asp	Thr	Leu	Met 235	Met	Trp	Trp	Phe	Cys 240
Glu	Phe	Cys	Ile	Trp 245	Arg	Arg	Leu	Trp	Met 250	Tyr	Ile	Phe	Glu	Trp 255	Leu
Ala	Tyr	Val	Asn 260	Cys	Pro	Cys	Ile	Asn 265	Pro	Ile	Thr	Tyr			

```
<210> 4
<211> 2095
<212> DNA
<213> Homo sapiens
```

<220>

<221> CDS

<222> (141) . . . (1883)

<400> 4

```
gtcgacccac gcgctccgcgg acgcgtgggc ggagggtttg aagcgcgcgc gccgagggagc 60
gaggtcgcag tgacagcggc gggcgatcgg acccaggctg cccgcgcgta cccgcctgcg 120
tccgcgcgtc ccgccccagc atg aca gcc ccg gcg ggt ccg cgc ggc tca gag 173
          Met Thr Ala Pro Ala Gly Pro Arg Gly Ser Glu
                1                5                10
```

acc gag cgg ctt ctg acc ccc aac ccc ggg tat ggg acc cag gcg ggg 221

Thr	Glu	Arg	Leu	Leu	Thr	Pro	Asn	Pro	Gly	Tyr	Gly	Thr	Gln	Ala	Gly		
			15					20					25				
cct	tca	ccg	gcc	cct	ccg	aca	ccc	cca	gaa	gag	gaa	gac	ctt	cgc	cgt	269	
Pro	Ser	Pro	Ala	Pro	Pro	Thr	Pro	Pro	Glu	Glu	Glu	Asp	Leu	Arg	Arg		
		30					35					40					
cgt	ctc	aaa	tac	ttt	ttc	atg	agt	ccc	tgc	gac	aag	ttt	cga	gcc	aag	317	
Arg	Leu	Lys	Tyr	Phe	Phe	Met	Ser	Pro	Cys	Asp	Lys	Phe	Arg	Ala	Lys		
	45					50					55						
ggc	cgc	aag	ccc	tgc	aag	ctg	atg	ctg	caa	gtg	gtc	aag	atc	ctg	gtg	365	
Gly	Arg	Lys	Pro	Cys	Lys	Leu	Met	Leu	Gln	Val	Val	Lys	Ile	Leu	Val		
	60				65					70					75		
gtc	acg	gtg	cag	ctc	atc	ctg	ttt	ggg	ctc	agt	aat	cag	ctg	gct	gtg	413	
Val	Thr	Val	Gln	Leu	Ile	Leu	Phe	Gly	Leu	Ser	Asn	Gln	Leu	Ala	Val		
			80						85					90			
aca	ttc	cgg	gaa	gag	aac	acc	atc	gcc	ttc	cga	cac	ctc	ttc	ctg	ctg	461	
Thr	Phe	Arg	Glu	Glu	Asn	Thr	Ile	Ala	Phe	Arg	His	Leu	Phe	Leu	Leu		
			95					100					105				
ggc	tac	tcg	gac	gga	gcg	gat	gac	acc	ttc	gca	gcc	tac	acg	cgg	gag	509	
Gly	Tyr	Ser	Asp	Gly	Ala	Asp	Asp	Thr	Phe	Ala	Ala	Tyr	Thr	Arg	Glu		
		110					115					120					
cag	ctg	tac	cag	gcc	atc	ttc	cat	gct	gtg	gac	cag	tac	ctg	gcg	ttg	557	
Gln	Leu	Tyr	Gln	Ala	Ile	Phe	His	Ala	Val	Asp	Gln	Tyr	Leu	Ala	Leu		
	125					130					135						
cct	gac	gtg	tca	ctg	ggc	cgg	tat	gcg	tat	gtc	cgt	ggg	ggg	ggg	gac	605	
Pro	Asp	Val	Ser	Leu	Gly	Arg	Tyr	Ala	Tyr	Val	Arg	Gly	Gly	Gly	Asp		
	140				145					150					155		
cct	tgg	acc	aat	ggc	tca	ggg	ctt	gct	ctc	tgc	cag	cgg	tac	tac	cac	653	
Pro	Trp	Thr	Asn	Gly	Ser	Gly	Leu	Ala	Leu	Cys	Gln	Arg	Tyr	Tyr	His		
				160					165					170			
cga	ggc	cac	gtg	gac	ccg	gcc	aac	gac	aca	ttt	gac	att	gat	ccg	atg	701	
Arg	Gly	His	Val	Asp	Pro	Ala	Asn	Asp	Thr	Phe	Asp	Ile	Asp	Pro	Met		
			175					180					185				
gtg	gtt	act	gac	tgc	atc	cag	gtg	gat	ccc	ccc	gag	cgg	ccc	cct	ccg	749	
Val	Val	Thr	Asp	Cys	Ile	Gln	Val	Asp	Pro	Pro	Glu	Arg	Pro	Pro	Pro		
		190					195					200					
ccc	ccc	agc	gac	gat	ctc	acc	ctc	ttg	gaa	agc	agc	tcc	agt	tac	aag	797	
Pro	Pro	Ser	Asp	Asp	Leu	Thr	Leu	Leu	Glu	Ser	Ser	Ser	Ser	Tyr	Lys		
		205				210					215						
aac	ctc	acg	ctc	aaa	ttc	cac	aag	ctg	gtc	aat	gtc	acc	atc	cac	ttc	845	
Asn	Leu	Thr	Leu	Lys	Phe	His	Lys	Leu	Val	Asn	Val	Thr	Ile	His	Phe		
	220				225					230					235		
cgg	ctg	aag	acc	att	aac	ctc	cag	agc	ctc	atc	aat	aat	gag	atc	ccg	893	
Arg	Leu	Lys	Thr	Ile	Asn	Leu	Gln	Ser	Leu	Ile	Asn	Asn	Glu	Ile	Pro		
				240					245					250			
gac	tgc	tat	acc	ttc	agc	gtc	ctg	atc	acg	ttt	gac	aac	aaa	gca	cac	941	
Asp	Cys	Tyr	Thr	Phe	Ser	Val	Leu	Ile	Thr	Phe	Asp	Asn	Lys	Ala	His		

255										260										265										
agt	ggg	cgg	atc	ccc	atc	agc	ctg	gag	acc	cag	gcc	cac	atc	cag	gag	989														
Ser	Gly	Arg	Ile	Pro	Ile	Ser	Leu	Glu	Thr	Gln	Ala	His	Ile	Gln	Glu															
		270						275					280																	
tgt	aag	cac	ccc	agt	gtc	ttc	cag	cac	gga	gac	aac	agc	ttc	cgg	ctc	1037														
Cys	Lys	His	Pro	Ser	Val	Phe	Gln	His	Gly	Asp	Asn	Ser	Phe	Arg	Leu															
	285					290					295																			
ctg	ttt	gac	gtg	gtg	gtc	atc	ctc	acc	tgc	tcc	ctg	tcc	ttc	ctc	ctc	1085														
Leu	Phe	Asp	Val	Val	Val	Ile	Leu	Thr	Cys	Ser	Leu	Ser	Phe	Leu	Leu															
300					305					310					315															
tgc	gcc	cgc	tca	ctc	ctt	cga	ggc	ttc	ctg	ctg	cag	aac	gag	ttt	gtg	1133														
Cys	Ala	Arg	Ser	Leu	Leu	Arg	Gly	Phe	Leu	Leu	Gln	Asn	Glu	Phe	Val															
				320					325					330																
ggg	ttc	atg	tgg	cgg	cag	cgg	gga	cgg	gtc	atc	agc	ctg	tgg	gag	cgg	1181														
Gly	Phe	Met	Trp	Arg	Gln	Arg	Gly	Cys	Val	Ile	Ser	Leu	Trp	Glu	Arg															
			335					340					345																	
ctg	gaa	ttt	gtc	aat	ggc	tgg	tac	atc	ctg	ctc	gtc	acc	agc	gat	gtg	1229														
Leu	Glu	Phe	Val	Asn	Gly	Trp	Tyr	Ile	Leu	Leu	Val	Thr	Ser	Asp	Val															
		350					355					360																		
ctc	acc	atc	tcg	ggc	acc	atc	atg	aag	atc	ggc	atc	gag	gcc	aag	aac	1277														
Leu	Thr	Ile	Ser	Gly	Thr	Ile	Met	Lys	Ile	Gly	Ile	Glu	Ala	Lys	Asn															
	365					370					375																			
ttg	gcg	agc	tac	gac	gtc	tgc	agc	atc	ctc	ctg	ggc	acc	tcg	acg	ctg	1325														
Leu	Ala	Ser	Tyr	Asp	Val	Cys	Ser	Ile	Leu	Leu	Gly	Thr	Ser	Thr	Leu															
380					385					390					395															
ctg	gtg	tgg	gtg	ggc	gtg	atc	cgc	tac	ctg	acc	ttc	ttc	cac	aac	tac	1373														
Leu	Val	Trp	Val	Gly	Val	Ile	Arg	Tyr	Leu	Thr	Phe	Phe	His	Asn	Tyr															
				400					405					410																
aat	atc	ctc	atc	gcc	aca	ctg	cgg	gtg	gcc	ctg	ccc	agc	gtc	atg	cgc	1421														
Asn	Ile	Leu	Ile	Ala	Thr	Leu	Arg	Val	Ala	Leu	Pro	Ser	Val	Met	Arg															
			415					420					425																	
ttc	tgc	tgc	tgc	gtg	gct	gtc	atc	tac	ctg	ggc	tac	tgc	ttc	tgt	ggc	1469														
Phe	Cys	Cys	Cys	Val	Ala	Val	Ile	Tyr	Leu	Gly	Tyr	Cys	Phe	Cys	Gly															
	430						435					440																		
tgg	atc	gtg	ctg	ggg	ccc	tat	cat	gtg	aag	ttc	cgc	tca	ctc	tcc	atg	1517														
Trp	Ile	Val	Leu	Gly	Pro	Tyr	His	Val	Lys	Phe	Arg	Ser	Leu	Ser	Met															
	445					450					455																			
gtg	tct	gag	tgc	ctg	ttc	tcg	ctc	atc	aat	ggg	gac	gac	atg	ttt	gtg	1565														
Val	Ser	Glu	Cys	Leu	Phe	Ser	Leu	Ile	Asn	Gly	Asp	Asp	Met	Phe	Val															
460					465					470					475															
acg	ttc	gcc	gcc	atg	cag	gcg	cag	cag	ggc	cgc	agc	agc	ctg	gtg	tgg	1613														
Thr	Phe	Ala	Ala	Met	Gln	Ala	Gln	Gln	Gly	Arg	Ser	Ser	Leu	Val	Trp															
				480					485					490																
ctc	ttc	tcc	cag	ctc	tac	ctt	tac	tcc	ttc	atc	agc	ctc	ttc	atc	tac	1661														
Leu	Phe	Ser	Gln	Leu	Tyr	Leu	Tyr	Ser	Phe	Ile	Ser	Leu	Phe	Ile	Tyr															
			495					500					505																	

```

atg gtg ctc agc ctc ttc atc gcg ctc atc acc ggc gcc tac gac acc 1709
Met Val Leu Ser Leu Phe Ile Ala Leu Ile Thr Gly Ala Tyr Asp Thr
510 515 520

atc aag cat ccc ggc ggc gca ggc gca gag gag agc gag ctg cag gcc 1757
Ile Lys His Pro Gly Gly Ala Gly Ala Glu Glu Ser Glu Leu Gln Ala
525 530 535

tac atc gca cag tgc cag gac agc ccc acc tcc ggc aag ttc cgc cgc 1805
Tyr Ile Ala Gln Cys Gln Asp Ser Pro Thr Ser Gly Lys Phe Arg Arg
540 545 550 555

ggg agc ggc tcg gcc tgc agc ctt ctc tgc tgc tgc gga agg gac ccc 1853
Gly Ser Gly Ser Ala Cys Ser Leu Leu Cys Cys Cys Gly Arg Asp Pro
560 565 570

tcg gag gag cat tcg ctg ctg gtg aat tga ttcgacctga ctgccgttgg 1903
Ser Glu Glu His Ser Leu Leu Val Asn *
575 580

accgtagggc ctggactgca gagacccccg ccccgacccc gcttatttat ttgtaggggtt 1963
tgcttttaag gatcggctcc ctgtcgcgcc cgaggagggc ctggaccttt cgtgtcggac 2023
ccttggggggc ggggagactg ggtgggaagg tgtgaataaa agggaaatta aaaaaaaaaa 2083
aaaaatttta aa 2095

```

```

<210> 5
<211> 580
<212> PRT
<213> Homo sapiens

```

```

<400> 5
Met Thr Ala Pro Ala Gly Pro Arg Gly Ser Glu Thr Glu Arg Leu Leu
1 5 10 15
Thr Pro Asn Pro Gly Tyr Gly Thr Gln Ala Gly Pro Ser Pro Ala Pro
20 25 30
Pro Thr Pro Pro Glu Glu Glu Asp Leu Arg Arg Arg Leu Lys Tyr Phe
35 40 45
Phe Met Ser Pro Cys Asp Lys Phe Arg Ala Lys Gly Arg Lys Pro Cys
50 55 60
Lys Leu Met Leu Gln Val Val Lys Ile Leu Val Val Thr Val Gln Leu
65 70 75 80
Ile Leu Phe Gly Leu Ser Asn Gln Leu Ala Val Thr Phe Arg Glu Glu
85 90 95
Asn Thr Ile Ala Phe Arg His Leu Phe Leu Leu Gly Tyr Ser Asp Gly
100 105 110
Ala Asp Asp Thr Phe Ala Ala Tyr Thr Arg Glu Gln Leu Tyr Gln Ala
115 120 125
Ile Phe His Ala Val Asp Gln Tyr Leu Ala Leu Pro Asp Val Ser Leu
130 135 140
Gly Arg Tyr Ala Tyr Val Arg Gly Gly Gly Asp Pro Trp Thr Asn Gly
145 150 155 160
Ser Gly Leu Ala Leu Cys Gln Arg Tyr Tyr His Arg Gly His Val Asp
165 170 175
Pro Ala Asn Asp Thr Phe Asp Ile Asp Pro Met Val Val Thr Asp Cys
180 185 190
Ile Gln Val Asp Pro Pro Glu Arg Pro Pro Pro Pro Ser Asp Asp
195 200 205
Leu Thr Leu Leu Glu Ser Ser Ser Ser Tyr Lys Asn Leu Thr Leu Lys
210 215 220
Phe His Lys Leu Val Asn Val Thr Ile His Phe Arg Leu Lys Thr Ile

```


225					230					235					240
Asn	Leu	Gln	Ser	Leu	Ile	Asn	Asn	Glu	Ile	Pro	Asp	Cys	Tyr	Thr	Phe
				245					250					255	
Ser	Val	Leu	Ile	Thr	Phe	Asp	Asn	Lys	Ala	His	Ser	Gly	Arg	Ile	Pro
		260						265					270		
Ile	Ser	Leu	Glu	Thr	Gln	Ala	His	Ile	Gln	Glu	Cys	Lys	His	Pro	Ser
		275						280				285			
Val	Phe	Gln	His	Gly	Asp	Asn	Ser	Phe	Arg	Leu	Leu	Phe	Asp	Val	Val
	290					295					300				
Val	Ile	Leu	Thr	Cys	Ser	Leu	Ser	Phe	Leu	Leu	Cys	Ala	Arg	Ser	Leu
305					310					315					320
Leu	Arg	Gly	Phe	Leu	Leu	Gln	Asn	Glu	Phe	Val	Gly	Phe	Met	Trp	Arg
				325					330					335	
Gln	Arg	Gly	Arg	Val	Ile	Ser	Leu	Trp	Glu	Arg	Leu	Glu	Phe	Val	Asn
			340					345					350		
Gly	Trp	Tyr	Ile	Leu	Leu	Val	Thr	Ser	Asp	Val	Leu	Thr	Ile	Ser	Gly
		355					360					365			
Thr	Ile	Met	Lys	Ile	Gly	Ile	Glu	Ala	Lys	Asn	Leu	Ala	Ser	Tyr	Asp
	370					375					380				
Val	Cys	Ser	Ile	Leu	Leu	Gly	Thr	Ser	Thr	Leu	Leu	Val	Trp	Val	Gly
385					390					395					400
Val	Ile	Arg	Tyr	Leu	Thr	Phe	Phe	His	Asn	Tyr	Asn	Ile	Leu	Ile	Ala
				405					410					415	
Thr	Leu	Arg	Val	Ala	Leu	Pro	Ser	Val	Met	Arg	Phe	Cys	Cys	Cys	Val
			420					425					430		
Ala	Val	Ile	Tyr	Leu	Gly	Tyr	Cys	Phe	Cys	Gly	Trp	Ile	Val	Leu	Gly
		435					440					445			
Pro	Tyr	His	Val	Lys	Phe	Arg	Ser	Leu	Ser	Met	Val	Ser	Glu	Cys	Leu
						455					460				
Phe	Ser	Leu	Ile	Asn	Gly	Asp	Asp	Met	Phe	Val	Thr	Phe	Ala	Ala	Met
465					470					475					480
Gln	Ala	Gln	Gln	Gly	Arg	Ser	Ser	Leu	Val	Trp	Leu	Phe	Ser	Gln	Leu
				485					490					495	
Tyr	Leu	Tyr	Ser	Phe	Ile	Ser	Leu	Phe	Ile	Tyr	Met	Val	Leu	Ser	Leu
			500					505					510		
Phe	Ile	Ala	Leu	Ile	Thr	Gly	Ala	Tyr	Asp	Thr	Ile	Lys	His	Pro	Gly
		515					520					525			
Gly	Ala	Gly	Ala	Glu	Glu	Ser	Glu	Leu	Gln	Ala	Tyr	Ile	Ala	Gln	Cys
		530				535					540				
Gln	Asp	Ser	Pro	Thr	Ser	Gly	Lys	Phe	Arg	Arg	Gly	Ser	Gly	Ser	Ala
545					550					555					560
Cys	Ser	Leu	Leu	Cys	Cys	Cys	Gly	Arg	Asp	Pro	Ser	Glu	Glu	His	Ser
				565					570					575	
Leu	Leu	Val	Asn												
			580												

<210> 6
 <211> 1743
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1743)

<400> 6																48
atg	aca	gcc	ccg	gcg	ggt	ccg	cgc	ggc	tca	gag	acc	gag	cgg	ctt	ctg	
Met	Thr	Ala	Pro	Ala	Gly	Pro	Arg	Gly	Ser	Glu	Thr	Glu	Arg	Leu	Leu	
1				5				10						15		

acc	ccc	aac	ccc	ggg	tat	ggg	acc	cag	gcg	ggg	cct	tca	ccg	gcc	cct	96
Thr	Pro	Asn	Pro	Gly	Tyr	Gly	Thr	Gln	Ala	Gly	Pro	Ser	Pro	Ala	Pro	
			20					25					30			
ccg	aca	ccc	cca	gaa	gag	gaa	gac	ctt	cgc	cgt	cgt	ctc	aaa	tac	ttt	144
Pro	Thr	Pro	Pro	Glu	Glu	Glu	Asp	Leu	Arg	Arg	Arg	Leu	Lys	Tyr	Phe	
		35					40					45				
ttc	atg	agt	ccc	tgc	gac	aag	ttt	cga	gcc	aag	ggc	cgc	aag	ccc	tgc	192
Phe	Met	Ser	Pro	Cys	Asp	Lys	Phe	Arg	Ala	Lys	Gly	Arg	Lys	Pro	Cys	
	50					55					60					
aag	ctg	atg	ctg	caa	gtg	gtc	aag	atc	ctg	gtg	gtc	acg	gtg	cag	ctc	240
Lys	Leu	Met	Leu	Gln	Val	Val	Lys	Ile	Leu	Val	Val	Thr	Val	Gln	Leu	
	65				70					75					80	
atc	ctg	ttt	ggg	ctc	agt	aat	cag	ctg	gct	gtg	aca	ttc	cgg	gaa	gag	288
Ile	Leu	Phe	Gly	Leu	Ser	Asn	Gln	Leu	Ala	Val	Thr	Phe	Arg	Glu	Glu	
			85					90						95		
aac	acc	atc	gcc	ttc	cga	cac	ctc	ttc	ctg	ctg	ggc	tac	tcg	gac	gga	336
Asn	Thr	Ile	Ala	Phe	Arg	His	Leu	Phe	Leu	Leu	Gly	Tyr	Ser	Asp	Gly	
			100					105					110			
gcg	gat	gac	acc	ttc	gca	gcc	tac	acg	cgg	gag	cag	ctg	tac	cag	gcc	384
Ala	Asp	Asp	Thr	Phe	Ala	Ala	Tyr	Thr	Arg	Glu	Gln	Leu	Tyr	Gln	Ala	
			115				120					125				
atc	ttc	cat	gct	gtg	gac	cag	tac	ctg	gcg	ttg	cct	gac	gtg	tca	ctg	432
Ile	Phe	His	Ala	Val	Asp	Gln	Tyr	Leu	Ala	Leu	Pro	Asp	Val	Ser	Leu	
	130				135						140					
ggc	cgg	tat	gcg	tat	gtc	cgt	ggt	ggg	ggt	gac	cct	tgg	acc	aat	ggc	480
Gly	Arg	Tyr	Ala	Tyr	Val	Arg	Gly	Gly	Gly	Asp	Pro	Trp	Thr	Asn	Gly	
	145				150					155					160	
tca	ggg	ctt	gct	ctc	tgc	cag	cgg	tac	tac	cac	cga	ggc	cac	gtg	gac	528
Ser	Gly	Leu	Ala	Leu	Cys	Gln	Arg	Tyr	Tyr	His	Arg	Gly	His	Val	Asp	
				165				170						175		
ccg	gcc	aac	gac	aca	ttt	gac	att	gat	ccg	atg	gtg	gtt	act	gac	tgc	576
Pro	Ala	Asn	Asp	Thr	Phe	Asp	Ile	Asp	Pro	Met	Val	Val	Thr	Asp	Cys	
			180					185					190			
atc	cag	gtg	gat	ccc	ccc	gag	cgg	ccc	cct	ccg	ccc	ccc	agc	gac	gat	624
Ile	Gln	Val	Asp	Pro	Pro	Glu	Arg	Pro	Pro	Pro	Pro	Pro	Ser	Asp	Asp	
		195					200					205				
ctc	acc	ctc	ttg	gaa	agc	agc	tcc	agt	tac	aag	aac	ctc	acg	ctc	aaa	672
Leu	Thr	Leu	Leu	Glu	Ser	Ser	Ser	Ser	Tyr	Lys	Asn	Leu	Thr	Leu	Lys	
	210				215						220					
ttc	cac	aag	ctg	gtc	aat	gtc	acc	atc	cac	ttc	cgg	ctg	aag	acc	att	720
Phe	His	Lys	Leu	Val	Asn	Val	Thr	Ile	His	Phe	Arg	Leu	Lys	Thr	Ile	
	225				230					235					240	
aac	ctc	cag	agc	ctc	atc	aat	aat	gag	atc	ccg	gac	tgc	tat	acc	ttc	768
Asn	Leu	Gln	Ser	Leu	Ile	Asn	Asn	Glu	Ile	Pro	Asp	Cys	Tyr	Thr	Phe	
				245				250						255		
agc	gtc	ctg	atc	acg	ttt	gac	aac	aaa	gca	cac	agt	ggg	cgg	atc	ccc	816

Ser	Val	Leu	Ile	Thr	Phe	Asp	Asn	Lys	Ala	His	Ser	Gly	Arg	Ile	Pro		
		260						265					270				
atc	agc	ctg	gag	acc	cag	gcc	cac	atc	cag	gag	tgt	aag	cac	ccc	agt	864	
Ile	Ser	Leu	Glu	Thr	Gln	Ala	His	Ile	Gln	Glu	Cys	Lys	His	Pro	Ser		
		275					280					285					
gtc	ttc	cag	cac	gga	gac	aac	agc	ttc	cgg	ctc	ctg	ttt	gac	gtg	gtg	912	
Val	Phe	Gln	His	Gly	Asp	Asn	Ser	Phe	Arg	Leu	Leu	Phe	Asp	Val	Val		
	290					295					300						
gtc	atc	ctc	acc	tgc	tcc	ctg	tcc	ttc	ctc	ctc	tgc	gcc	cgc	tca	ctc	960	
Val	Ile	Leu	Thr	Cys	Ser	Leu	Ser	Phe	Leu	Leu	Cys	Ala	Arg	Ser	Leu		
305					310					315					320		
ctt	cga	ggc	ttc	ctg	ctg	cag	aac	gag	ttt	gtg	ggg	ttc	atg	tgg	cgg	1008	
Leu	Arg	Gly	Phe	Leu	Leu	Gln	Asn	Glu	Phe	Val	Gly	Phe	Met	Trp	Arg		
			325					330						335			
cag	cgg	gga	cgg	gtc	atc	agc	ctg	tgg	gag	cgg	ctg	gaa	ttt	gtc	aat	1056	
Gln	Arg	Gly	Arg	Val	Ile	Ser	Leu	Trp	Glu	Arg	Leu	Glu	Phe	Val	Asn		
			340					345					350				
ggc	tgg	tac	atc	ctg	ctc	gtc	acc	agc	gat	gtg	ctc	acc	atc	tcg	ggc	1104	
Gly	Trp	Tyr	Ile	Leu	Leu	Val	Thr	Ser	Asp	Val	Leu	Thr	Ile	Ser	Gly		
		355					360					365					
acc	atc	atg	aag	atc	ggc	atc	gag	gcc	aag	aac	ttg	gcg	agc	tac	gac	1152	
Thr	Ile	Met	Lys	Ile	Gly	Ile	Glu	Ala	Lys	Asn	Leu	Ala	Ser	Tyr	Asp		
	370					375					380						
gtc	tgc	agc	atc	ctc	ctg	ggc	acc	tcg	acg	ctg	ctg	gtg	tgg	gtg	ggc	1200	
Val	Cys	Ser	Ile	Leu	Leu	Gly	Thr	Ser	Thr	Leu	Leu	Val	Trp	Val	Gly		
385					390					395					400		
gtg	atc	cgc	tac	ctg	acc	ttc	ttc	cac	aac	tac	aat	atc	ctc	atc	gcc	1248	
Val	Ile	Arg	Tyr	Leu	Thr	Phe	Phe	His	Asn	Tyr	Asn	Ile	Leu	Ile	Ala		
				405					410					415			
aca	ctg	cgg	gtg	gcc	ctg	ccc	agc	gtc	atg	cgc	ttc	tgc	tgc	tgc	gtg	1296	
Thr	Leu	Arg	Val	Ala	Leu	Pro	Ser	Val	Met	Arg	Phe	Cys	Cys	Cys	Val		
			420					425					430				
gct	gtc	atc	tac	ctg	ggc	tac	tgc	ttc	tgt	ggc	tgg	atc	gtg	ctg	ggg	1344	
Ala	Val	Ile	Tyr	Leu	Gly	Tyr	Cys	Phe	Cys	Gly	Trp	Ile	Val	Leu	Gly		
		435					440					445					
ccc	tat	cat	gtg	aag	ttc	cgc	tca	ctc	tcc	atg	gtg	tct	gag	tgc	ctg	1392	
Pro	Tyr	His	Val	Lys	Phe	Arg	Ser	Leu	Ser	Met	Val	Ser	Glu	Cys	Leu		
	450					455					460						
ttc	tcg	ctc	atc	aat	ggg	gac	gac	atg	ttt	gtg	acg	ttc	gcc	gcc	atg	1440	
Phe	Ser	Leu	Ile	Asn	Gly	Asp	Asp	Met	Phe	Val	Thr	Phe	Ala	Ala	Met		
465					470					475					480		
cag	gcg	cag	cag	ggc	cgc	agc	agc	ctg	gtg	tgg	ctc	ttc	tcc	cag	ctc	1488	
Gln	Ala	Gln	Gln	Gly	Arg	Ser	Ser	Leu	Val	Trp	Leu	Phe	Ser	Gln	Leu		
				485					490					495			
tac	ctt	tac	tcc	ttc	atc	agc	ctc	ttc	atc	tac	atg	gtg	ctc	agc	ctc	1536	
Tyr	Leu	Tyr	Ser	Phe	Ile	Ser	Leu	Phe	Ile	Tyr	Met	Val	Leu	Ser	Leu		

500	505	510	
ttc atc gcg ctc atc acc ggc gcc tac gac acc atc aag cat ccc ggc			1584
Phe Ile Ala Leu Ile Thr Gly Ala Tyr Asp Thr Ile Lys His Pro Gly			
515	520	525	
ggc gca ggc gca gag gag agc gag ctg cag gcc tac atc gca cag tgc			1632
Gly Ala Gly Ala Glu Glu Ser Glu Leu Gln Ala Tyr Ile Ala Gln Cys			
530	535	540	
cag gac agc ccc acc tcc ggc aag ttc cgc cgc ggg agc ggc tcg gcc			1680
Gln Asp Ser Pro Thr Ser Gly Lys Phe Arg Arg Gly Ser Gly Ser Ala			
545	550	555	560
tgc agc ctt ctc tgc tgc tgc gga agg gac ccc tcg gag gag cat tcg			1728
Cys Ser Leu Leu Cys Cys Cys Gly Arg Asp Pro Ser Glu Glu His Ser			
565	570	575	
ctg ctg gtg aat tga			1743
Leu Leu Val Asn *			
580			

<210> 7
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> N-Glycosylation site
 <221> VARIANT
 <222> (2)...(2)
 <223> Xaa = Any Amino Acid

<221> VARIANT
 <222> (3)...(3)
 <223> Xaa = Ser or Thr

<400> 7
 Asn Xaa Xaa
 1

<210> 8
 <211> 50
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 31K RNA-4 protein domain

<400> 8
 Val Trp Ile Leu Leu Leu Thr Ser Ser Thr Cys Tyr Gly Tyr His Asp
 1 5 10 15
 Val Val Val Asp Ile Glu Gln Cys Thr Leu Pro Ser Asn Ile Asp Gly
 20 25 30
 Cys Val Cys Cys Ser Gly Val Cys Tyr Phe Asn Asp Asn His Cys Phe
 35 40 45
 Cys Gly
 50

<210> 9
 <211> 839
 <212> PRT
 <213> Homo sapiens

<400> 9
 Met Lys Lys Trp Ser Ser Thr Asp Leu Gly Ala Ala Ala Asp Pro Leu
 1 5 10 15
 Gln Lys Asp Thr Cys Pro Asp Pro Leu Asp Gly Asp Pro Asn Ser Arg
 20 25 30
 Pro Pro Pro Ala Lys Pro Gln Leu Ser Thr Ala Lys Ser Arg Thr Arg
 35 40 45
 Leu Phe Gly Lys Gly Asp Ser Glu Glu Ala Phe Pro Val Asp Cys Pro
 50 55 60
 His Glu Glu Gly Glu Leu Asp Ser Cys Pro Thr Ile Thr Val Ser Pro
 65 70 75 80
 Val Ile Thr Ile Gln Arg Pro Gly Asp Gly Pro Thr Gly Ala Arg Leu
 85 90 95
 Leu Ser Gln Asp Ser Val Ala Ala Ser Thr Glu Lys Thr Leu Arg Leu
 100 105 110
 Tyr Asp Arg Arg Ser Ile Phe Glu Ala Val Ala Gln Asn Asn Cys Gln
 115 120 125
 Asp Leu Glu Ser Leu Leu Leu Phe Leu Gln Lys Ser Lys Lys His Leu
 130 135 140
 Thr Asp Asn Glu Phe Lys Asp Pro Glu Thr Gly Lys Thr Cys Leu Leu
 145 150 155 160
 Lys Ala Met Leu Asn Leu His Asp Gly Gln Asn Thr Thr Ile Pro Leu
 165 170 175
 Leu Leu Glu Ile Ala Arg Gln Thr Asp Ser Leu Lys Glu Leu Val Asn
 180 185 190
 Ala Ser Tyr Thr Asp Ser Tyr Tyr Lys Gly Gln Thr Ala Leu His Ile
 195 200 205
 Ala Ile Glu Arg Arg Asn Met Ala Leu Val Thr Leu Leu Val Glu Asn
 210 215 220
 Gly Ala Asp Val Gln Ala Ala His Gly Asp Phe Phe Lys Lys Thr
 225 230 235 240
 Lys Gly Arg Pro Gly Phe Tyr Phe Gly Glu Leu Pro Leu Ser Leu Ala
 245 250 255
 Ala Cys Thr Asn Gln Leu Gly Ile Val Lys Phe Leu Leu Gln Asn Ser
 260 265 270
 Trp Gln Thr Ala Asp Ile Ser Ala Arg Asp Ser Val Gly Asn Thr Val
 275 280 285
 Leu His Ala Leu Val Glu Val Ala Asp Asn Thr Ala Asp Asn Thr Lys
 290 295 300
 Phe Val Thr Ser Met Tyr Asn Glu Ile Leu Ile Leu Gly Ala Lys Leu
 305 310 315 320
 His Pro Thr Leu Lys Leu Glu Glu Leu Thr Asn Lys Lys Gly Met Thr
 325 330 335
 Pro Leu Ala Leu Ala Ala Gly Thr Gly Lys Ile Gly Val Leu Ala Tyr
 340 345 350
 Ile Leu Gln Arg Glu Ile Gln Glu Pro Glu Cys Arg His Leu Ser Arg
 355 360 365
 Lys Phe Thr Glu Trp Ala Tyr Gly Pro Val His Ser Ser Leu Tyr Asp
 370 375 380
 Leu Ser Cys Ile Asp Thr Cys Glu Lys Asn Ser Val Leu Glu Val Ile
 385 390 395 400
 Ala Tyr Ser Ser Ser Glu Thr Pro Asn Arg His Asp Met Leu Leu Val
 405 410 415
 Glu Pro Leu Asn Arg Leu Leu Gln Asp Lys Trp Asp Arg Phe Val Lys

<221> VARIANT
 <222> (667)...(667)
 <223> Xaa = Any Amino Acid

<400> 10

Met	Thr	Ser	Pro	Ser	Ser	Ser	Pro	Val	Phe	Arg	Leu	Glu	Thr	Leu	Asp
1				5					10					15	
Gly	Gly	Gln	Glu	Asp	Gly	Ser	Glu	Ala	Asp	Arg	Gly	Lys	Leu	Asp	Phe
			20					25					30		
Gly	Ser	Gly	Leu	Pro	Pro	Met	Glu	Ser	Gln	Phe	Gln	Gly	Glu	Asp	Arg
		35					40					45			
Lys	Phe	Ala	Ser	Gln	Ile	Arg	Val	Asn	Leu	Asn	Tyr	Arg	Lys	Gly	Thr
	50					55					60				
Gly	Ala	Ser	Gln	Pro	Asp	Pro	Asn	Arg	Phe	Asp	Arg	Asp	Arg	Leu	Phe
65					70					75					80
Asn	Val	Val	Ser	Arg	Gly	Val	Pro	Glu	Asp	Leu	Ala	Gly	Leu	Pro	Glu
			85						90					95	
Tyr	Leu	Ser	Lys	Thr	Ser	Lys	Tyr	Leu	Thr	Asp	Ser	Glu	Tyr	Thr	Glu
			100					105					110		
Gly	Ser	Thr	Gly	Lys	Thr	Cys	Leu	Met	Lys	Ala	Val	Leu	Asn	Leu	Lys
		115					120					125			
Asp	Gly	Val	Asn	Ala	Cys	Ile	Leu	Pro	Leu	Leu	Gln	Ile	Asp	Arg	Asp
	130					135					140				
Ser	Gly	Asn	Pro	Gln	Pro	Leu	Val	Asn	Ala	Gln	Cys	Thr	Asp	Asp	Tyr
145					150					155					160
Tyr	Arg	Gly	His	Ser	Ala	Leu	His	Ile	Ala	Ile	Glu	Lys	Arg	Ser	Leu
			165						170					175	
Gln	Cys	Val	Lys	Leu	Leu	Val	Glu	Asn	Gly	Ala	Asn	Val	His	Ala	Arg
			180					185					190		
Ala	Cys	Gly	Arg	Phe	Phe	Gln	Asn	Gly	Gln	Gly	Thr	Cys	Phe	Tyr	Phe
		195					200					205			
Gly	Glu	Leu	Pro	Leu	Ser	Leu	Ala	Ala	Cys	Thr	Lys	Gln	Trp	Asp	Val
	210					215					220				
Val	Ser	Tyr	Leu	Leu	Glu	Asn	Pro	His	Gln	Pro	Ala	Ser	Leu	Gln	Ala
225					230					235					240
Thr	Asp	Ser	Gln	Gly	Asn	Thr	Val	Leu	His	Ala	Leu	Val	Met	Ile	Ser
			245						250					255	
Asp	Asn	Ser	Ala	Glu	Asn	Ile	Ala	Leu	Val	Thr	Ser	Met	Tyr	Asp	Gly
			260					265					270		
Leu	Leu	Gln	Ala	Gly	Ala	Arg	Leu	Cys	Pro	Thr	Val	Gln	Leu	Glu	Asp
		275					280					285			
Ile	Arg	Asn	Leu	Gln	Asp	Leu	Thr	Pro	Leu	Lys	Leu	Ala	Ala	Lys	Glu
	290					295					300				
Gly	Lys	Ile	Glu	Ile	Phe	Arg	His	Ile	Leu	Gln	Arg	Glu	Phe	Ser	Gly
305					310					315					320
Leu	Ser	His	Leu	Ser	Arg	Lys	Phe	Thr	Glu	Trp	Cys	Tyr	Gly	Pro	Val
			325						330					335	
Arg	Val	Ser	Leu	Tyr	Asp	Leu	Ala	Ser	Val	Asp	Ser	Cys	Glu	Glu	Asn
			340					345					350		
Ser	Val	Leu	Glu	Ile	Ile	Ala	Phe	His	Cys	Lys	Ser	Pro	His	Arg	His
		355					360					365			
Arg	Met	Val	Val	Leu	Glu	Pro	Leu	Asn	Lys	Leu	Leu	Gln	Ala	Lys	Trp
	370					375						380			
Asp	Leu	Leu	Ile	Pro	Lys	Phe	Phe	Leu	Asn	Phe	Leu	Cys	Asn	Leu	Ile
385					390					395					400
Tyr	Met	Phe	Ile	Phe	Thr	Ala	Val	Ala	Tyr	His	Gln	Pro	Thr	Leu	Lys
			405						410					415	
Lys	Gln	Ala	Ala	Pro	His	Leu	Lys	Ala	Glu	Val	Gly	Asn	Ser	Met	Leu
		420						425					430		
Leu	Thr	Gly	His	Ile	Leu	Ile	Leu	Leu	Gly	Gly	Ile	Tyr	Leu	Leu	Val
		435					440					445			

Gly	Gln	Leu	Trp	Tyr	Phe	Trp	Arg	Arg	His	Leu	Phe	Ile	Trp	Ile	Ser
450						455				460					
Tyr	Thr	Asp	Ser	Tyr	Phe	Glu	Ile	Leu	Phe	Leu	Phe	His	Ser	Leu	Leu
465					470					475					480
Thr	Val	Val	Ser	Leu	Val	Leu	Cys	Phe	Leu	Val	Ile	Glu	Trp	Tyr	Leu
				485					490					495	
Pro	Leu	Leu	Val	Ser	Ala	Leu	Val	Leu	Gly	Trp	Leu	Asn	Leu	Leu	Tyr
			500					505					510		
Tyr	Thr	Arg	Gly	Phe	Gln	His	Thr	Gly	Ile	Tyr	Ser	Val	Met	Ile	Gln
		515					520					525			
Lys	Val	Ile	Leu	Arg	Asp	Met	Val	Arg	Phe	Leu	Val	Ile	Tyr	Leu	Val
	530					535					540				
Phe	Leu	Phe	Gly	Phe	Ala	Val	Ala	Leu	Val	Ser	Leu	Ser	Gln	Glu	Ala
545					550					555					560
Trp	Arg	Pro	Glu	Ala	Pro	Thr	Gly	Pro	Asn	Ala	Thr	Glu	Ser	Val	Gln
				565					570					575	
Pro	Met	Glu	Gly	Gln	Glu	Asp	Glu	Gly	Asn	Gly	Ala	Gln	Tyr	Arg	Gly
			580					585					590		
Ile	Leu	Glu	Ala	Ser	Leu	Glu	Leu	Phe	Lys	Phe	Thr	Ile	Gly	Met	Gly
	595						600					605			
Glu	Leu	Ala	Phe	Gln	Glu	Gln	Leu	His	Phe	Arg	Gly	Met	Val	Leu	Leu
	610					615					620				
Leu	Leu	Leu	Ala	Tyr	Val	Leu	Leu	Thr	Tyr	Ile	Leu	Leu	Leu	Asn	Met
625					630					635					640
Leu	Ile	Ala	Leu	Met	Ser	Glu	Thr	Val	Asn	Ser	Val	Ala	Thr	Asp	Ser
				645					650					655	
Trp	Ser	Ile	Trp	Lys	Leu	Gln	Lys	Ala	Ile	Xaa	Val	Leu	Glu	Met	Glu
			660					665					670		
Asn	Gly	Tyr	Trp	Trp	Cys	Arg	Lys	Lys	Gln	Arg	Ala	Gly	Val	Met	Leu
	675						680					685			
Thr	Val	Gly	Thr	Lys	Pro	Asp	Gly	Ser	Pro	Asp	Glu	Arg	Trp	Cys	Phe
	690					695					700				
Arg	Val	Glu	Glu	Val	Asn	Trp	Ala	Ser	Trp	Glu	Gln	Thr	Leu	Pro	Thr
705					710					715					720
Leu	Cys	Glu	Asp	Pro	Ser	Gly	Ala	Gly	Val	Pro	Arg	Thr	Leu	Glu	Asn
				725					730					735	
Pro	Val	Leu	Ala	Ser	Pro	Pro	Lys	Glu	Asp	Glu	Asp	Gly	Ala	Ser	Glu
			740					745					750		
Glu	Asn	Tyr	Val	Pro	Val	Gln	Leu	Leu	Gln	Ser	Asn				
	755						760								

<210> 11
 <211> 966
 <212> PRT
 <213> Mus musculus

<400> 11															
Met	Val	Asn	Ser	Arg	Arg	Val	Gln	Pro	Gln	Pro	Pro	Gly	Asp	Ala	Gly
1				5					10					15	
Arg	Ser	Pro	Ala	Pro	Arg	Ala	Ser	Gly	Pro	Gly	Arg	Leu	Val	Ala	Gly
			20					25					30		
Gly	Ala	Gly	Leu	Ala	Val	Pro	Gly	Gly	Leu	Gly	Glu	Gln	Arg	Gly	Leu
		35					40					45			
Glu	Ile	Glu	Met	Glu	Arg	Ile	Arg	Gln	Ala	Ala	Ala	Arg	Asp	Pro	Pro
	50					55					60				
Ala	Gly	Ala	Ser	Ala	Ser	Pro	Ser	Pro	Pro	Leu	Ser	Ser	Cys	Ser	Arg
65					70					75					80
Gln	Ala	Trp	Ser	Arg	Asp	Asn	Pro	Gly	Phe	Glu	Ala	Glu	Glu	Asp	Asp
				85				90						95	
Asp	Asp	Asp	Glu	Val	Glu	Gly	Glu	Glu	Gly	Gly	Met	Val	Val	Glu	Met

Lys Asp Leu Phe Gly Phe Thr Ile Met Phe Ser Ile Ile Phe Leu Ala
 595 600 605
 Tyr Ala Gln Leu Ala Tyr Leu Val Phe Gly Thr Gln Val Asp Asp Phe
 610 615 620
 Ser Thr Phe Gln Glu Cys Ile Phe Thr Gln Phe Arg Ile Ile Leu Gly
 625 630 635 640
 Asp Ile Asn Phe Ala Glu Ile Glu Glu Ala Asn Arg Val Leu Gly Pro
 645 650 655
 Leu Tyr Phe Thr Thr Phe Val Phe Phe Met Phe Phe Ile Leu Leu Asn
 660 665 670
 Met Phe Leu Ala Ile Ile Asn Asp Ser Tyr Ser Glu Val Lys Ser Asp
 675 680 685
 Leu Ala Gln Gln Lys Ala Glu Met Glu Leu Ser Asp Leu Ile Arg Lys
 690 695 700
 Gly Cys Gln Lys Ala Leu Val Lys Leu Lys Leu Lys Arg Asn Thr Val
 705 710 715 720
 Asp Ala Ile Ser Glu Ser Leu Arg Gln Gly Gly Gly Lys Leu Asn Phe
 725 730 735
 Asp Glu Leu Arg Gln Asp Leu Lys Gly Lys Gly His Thr Asp Ala Glu
 740 745 750
 Ile Glu Ala Ile Phe Thr Lys Tyr Asp Gln Asp Gly Asp Gln Glu Leu
 755 760 765
 Thr Glu Arg Glu His Gln Gln Met Arg Asp Asp Leu Glu Lys Glu Arg
 770 775 780
 Glu Asp Leu Asp Leu Glu His Ser Ser Leu Pro Arg Pro Met Ser Ser
 785 790 795 800
 Arg Ser Phe Pro Arg Ser Leu Asp Asp Ser Glu Glu Glu Asp Asp Glu
 805 810 815
 Asp Ser Gly His Ser Ser Arg Arg Arg Gly Ser Ile Ser Ser Gly Val
 820 825 830
 Ser Tyr Glu Glu Phe Gln Val Leu Val Arg Arg Val Asp Arg Met Glu
 835 840 845
 His Ser Ile Gly Ser Ile Val Ser Lys Ile Asp Ala Val Ile Val Lys
 850 855 860
 Leu Glu Ile Met Glu Arg Ala Lys Leu Lys Arg Arg Glu Val Leu Gly
 865 870 875 880
 Arg Leu Leu Asp Gly Val Ala Glu Asp Ala Arg Leu Gly Arg Asp Ser
 885 890 895
 Glu Ile His Arg Glu Gln Met Glu Arg Leu Val Arg Glu Glu Leu Glu
 900 905 910
 Arg Trp Glu Ser Asp Asp Ala Ala Ser Gln Thr Gly His Gly Val Ser
 915 920 925
 Thr Gln Val Gly Leu Gly Gly Gln Pro His Pro Arg Asn Ser Arg Pro
 930 935 940
 Pro Ser Ser Gln Ser Ala Glu Gly Leu Glu Gly Gly Ser Gly Asn Gly
 945 950 955 960
 Ser Ala Asn Val His Ala
 965

<210> 12
 <211> 1533
 <212> PRT
 <213> Homo sapiens

<400> 12
 Met Tyr Ile Arg Val Ser Tyr Asp Thr Lys Pro Asp Ser Leu Leu His
 1 5 10 15
 Leu Met Val Lys Asp Trp Gln Leu Glu Leu Pro Lys Leu Leu Ile Ser
 20 25 30
 Val His Gly Gly Leu Gln Asn Phe Glu Met Gln Pro Lys Leu Lys Gln

Asp	Val	Asp	Asp	Pro	Ala	Val	Ser	Arg	Phe	Gln	Tyr	Pro	Phe	His	Glu
530						535					540				
Leu	Met	Val	Trp	Ala	Val	Leu	Met	Lys	Arg	Gln	Lys	Met	Ala	Val	Phe
545				550						555					560
Leu	Trp	Gln	Arg	Gly	Glu	Glu	Ser	Met	Ala	Lys	Ala	Leu	Val	Ala	Cys
				565					570					575	
Lys	Leu	Tyr	Lys	Ala	Met	Ala	His	Glu	Ser	Ser	Glu	Ser	Asp	Leu	Val
			580					585					590		
Asp	Asp	Ile	Ser	Gln	Asp	Leu	Asp	Asn	Asn	Ser	Lys	Asp	Phe	Gly	Gln
		595					600					605			
Leu	Ala	Leu	Glu	Leu	Leu	Asp	Gln	Ser	Tyr	Lys	His	Asp	Glu	Gln	Ile
	610					615					620				
Ala	Met	Lys	Leu	Leu	Thr	Tyr	Glu	Leu	Lys	Asn	Trp	Ser	Asn	Ser	Thr
625					630					635					640
Cys	Leu	Lys	Leu	Ala	Val	Ala	Ala	Lys	His	Arg	Asp	Phe	Ile	Ala	His
				645					650					655	
Thr	Cys	Ser	Gln	Met	Leu	Leu	Thr	Asp	Met	Trp	Met	Gly	Arg	Leu	Arg
			660					665					670		
Met	Arg	Lys	Asn	Pro	Gly	Leu	Lys	Val	Ile	Met	Gly	Ile	Leu	Leu	Pro
			675				680					685			
Pro	Thr	Ile	Leu	Phe	Leu	Glu	Phe	Arg	Thr	Tyr	Asp	Asp	Phe	Ser	Tyr
	690					695					700				
Gln	Thr	Ser	Lys	Glu	Asn	Glu	Asp	Gly	Lys	Glu	Lys	Glu	Glu	Glu	Asn
705					710					715					720
Thr	Asp	Ala	Asn	Ala	Asp	Ala	Gly	Ser	Arg	Lys	Gly	Asp	Glu	Glu	Asn
				725					730					735	
Glu	His	Lys	Lys	Gln	Arg	Ser	Ile	Pro	Ile	Gly	Thr	Lys	Ile	Cys	Glu
			740					745					750		
Phe	Tyr	Asn	Ala	Pro	Ile	Val	Lys	Phe	Trp	Phe	Tyr	Thr	Ile	Ser	Tyr
		755					760					765			
Leu	Gly	Tyr	Leu	Leu	Leu	Phe	Asn	Tyr	Val	Ile	Leu	Val	Arg	Met	Asp
	770					775					780				
Gly	Trp	Pro	Ser	Leu	Gln	Glu	Trp	Ile	Val	Ile	Ser	Tyr	Ile	Val	Ser
785					790					795					800
Leu	Ala	Leu	Glu	Lys	Ile	Arg	Glu	Ile	Leu	Met	Ser	Glu	Pro	Gly	Lys
				805					810					815	
Leu	Ser	Gln	Lys	Ile	Lys	Val	Trp	Leu	Gln	Glu	Tyr	Trp	Asn	Ile	Thr
			820					825					830		
Asp	Leu	Val	Ala	Ile	Ser	Thr	Phe	Met	Ile	Gly	Ala	Ile	Leu	Arg	Leu
		835					840					845			
Gln	Asn	Gln	Pro	Tyr	Met	Gly	Tyr	Gly	Arg	Val	Ile	Tyr	Cys	Val	Asp
	850					855					860				
Ile	Ile	Phe	Trp	Tyr	Ile	Arg	Val	Leu	Asp	Ile	Phe	Gly	Val	Asn	Lys
865					870					875					880
Tyr	Leu	Gly	Pro	Tyr	Val	Met	Met	Ile	Gly	Lys	Met	Met	Ile	Asp	Met
				885					890					895	
Leu	Tyr	Phe	Val	Val	Ile	Met	Leu	Val	Val	Leu	Met	Ser	Phe	Gly	Val
			900					905					910		
Ala	Arg	Gln	Ala	Ile	Leu	His	Pro	Glu	Glu	Lys	Pro	Ser	Trp	Lys	Leu
			915				920						925		
Ala	Arg	Asn	Ile	Phe	Tyr	Met	Pro	Tyr	Trp	Met	Ile	Tyr	Gly	Glu	Val
	930					935					940				
Phe	Ala	Asp	Gln	Ile	Asp	Leu	Tyr	Ala	Met	Glu	Ile	Asn	Pro	Pro	Cys
945					950					955					960
Gly	Glu	Asn	Leu	Tyr	Asp	Glu	Glu	Gly	Lys	Arg	Leu	Pro	Pro	Cys	Ile
				965					970					975	
Pro	Gly	Ala	Trp	Leu	Thr	Pro	Ala	Leu	Met	Ala	Cys	Tyr	Leu	Leu	Val
			980					985					990		
Ala	Asn	Ile	Leu	Leu	Val	Asn	Leu	Leu	Ile	Ala	Val	Phe	Asn	Asn	Thr
			995				1000					1005			
Phe	Phe	Glu	Val	Lys	Ser	Ile	Ser	Asn	Gln	Val	Trp	Lys	Phe	Gln	Arg

1010	1015	1020
Tyr Gln Leu Ile Met Thr Phe His Asp Arg Pro Val Leu Pro Pro Pro		
1025	1030	1035
Met Ile Ile Leu Ser His Ile Tyr Ile Ile Ile Met Arg Leu Ser Gly		1040
	1045	1050
Arg Cys Arg Lys Lys Arg Glu Gly Asp Gln Glu Glu Arg Asp Arg Gly		1055
	1060	1065
Leu Lys Leu Phe Leu Ser Asp Glu Glu Leu Lys Arg Leu His Glu Phe		1070
	1075	1080
Glu Glu Gln Cys Val Gln Glu His Phe Arg Glu Lys Glu Asp Glu Gln		1085
	1090	1095
Gln Ser Ser Ser Asp Glu Arg Ile Arg Val Thr Ser Glu Arg Val Glu		1100
1105	1110	1115
Asn Met Ser Met Arg Leu Glu Glu Ile Asn Glu Arg Glu Thr Phe Met		1120
	1125	1130
Lys Thr Ser Leu Gln Thr Val Asp Leu Arg Leu Ala Gln Leu Glu Glu		1135
	1140	1145
Leu Ser Asn Arg Met Val Asn Ala Leu Glu Asn Leu Ala Gly Ile Asp		1150
	1155	1160
Arg Ser Asp Leu Ile Gln Ala Arg Ser Arg Ala Ser Ser Glu Cys Glu		1165
	1170	1175
Ala Thr Tyr Leu Leu Arg Gln Ser Ser Ile Asn Ser Ala Asp Gly Tyr		1180
1185	1190	1195
Ser Leu Tyr Arg Tyr His Phe Asn Gly Glu Glu Leu Leu Phe Glu Asp		1200
	1205	1210
Thr Ser Leu Ser Thr Ser Pro Gly Thr Gly Val Arg Lys Lys Thr Cys		1215
	1220	1225
Ser Phe Arg Ile Lys Glu Glu Lys Asp Val Lys Thr His Leu Val Pro		1230
	1235	1240
Glu Cys Gln Asn Ser Leu His Leu Ser Leu Gly Thr Ser Thr Ser Ala		1245
	1250	1255
Thr Pro Asp Gly Ser His Leu Ala Val Asp Asp Leu Lys Asn Ala Glu		1260
1265	1270	1275
Glu Ser Lys Leu Gly Pro Asp Ile Gly Ile Ser Lys Glu Asp Asp Glu		1280
	1285	1290
Arg Gln Thr Asp Ser Lys Lys Glu Glu Thr Ile Ser Pro Ser Leu Asn		1295
	1300	1305
Lys Thr Asp Val Ile His Gly Gln Asp Lys Ser Asp Val Gln Asn Thr		1310
	1315	1320
Gln Leu Thr Val Glu Thr Thr Asn Ile Glu Gly Thr Ile Ser Tyr Pro		1325
	1330	1335
Leu Glu Glu Thr Lys Ile Thr Arg Tyr Phe Pro Asp Glu Thr Ile Asn		1340
1345	1350	1355
Ala Cys Lys Thr Met Lys Ser Arg Ser Phe Val Tyr Ser Arg Gly Arg		1360
	1365	1370
Lys Leu Val Gly Gly Val Asn Gln Asp Val Glu Tyr Ser Ser Ile Thr		1375
	1380	1385
Asp Gln Gln Leu Thr Thr Glu Trp Gln Cys Gln Val Gln Lys Ile Thr		1390
	1395	1400
Arg Ser His Ser Thr Asp Ile Pro Tyr Ile Val Ser Glu Ala Ala Val		1405
	1410	1415
Gln Ala Glu Gln Lys Glu Gln Phe Ala Asp Met Gln Asp Glu His His		1420
1425	1430	1435
Val Ala Glu Ala Ile Pro Arg Ile Pro Arg Leu Ser Leu Thr Ile Thr		1440
	1445	1450
Asp Arg Asn Gly Met Glu Asn Leu Leu Ser Val Lys Pro Asp Gln Thr		1455
	1460	1465
Leu Gly Phe Pro Ser Leu Arg Ser Lys Ser Leu His Gly His Pro Arg		1470
	1475	1480
Asn Val Lys Ser Ile Gln Gly Lys Leu Asp Arg Ser Gly His Ala Ser		1485
1490	1495	1500

Ser Val Ser Ser Leu Val Ile Val Ser Gly Met Thr Ala Glu Glu Lys
 1505 1510 1515 1520
 Lys Val Lys Lys Glu Lys Ala Ser Thr Glu Thr Glu Cys
 1525 1530

<210> 13
 <211> 4052
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (459)...(1592)

<400> 13
 ccaagatttta aagcccgcga gttttgttct tgagaccagc gacttttagct ccgatgcggg 60
 aaggaaagcc gacctccgat ttggacattt aaagagctgg gcttgaactt cgtgagtttc 120
 gctctaaact gcccttgaaa tgaagctgga cttggagggtg gcatggaata ttcacatggg 180
 agagccgcat gaggccgccc accacgcttc ctgaaggatg cccgtgtgga agaattttga 240
 cgtgccagtg tcctcgttct acaggggtgtt ccattcttcc gcaatctcag aaaaatggga 300
 ctaaaagaaa ctatttttga aaataagaag acttccattt ttaatgacca acatgtatta 360
 agatggacac ctactctacg aaacacgaag ttctatgggc tcgaagaagc ccgtgcctgt 420
 ttaaaactga tcctaactaa aaacagactt gagtggat atg aga atg ttg gtt agt 476
 Met Arg Met Leu Val Ser
 1 5
 ggc aga aga gtc aaa aaa tgg cag tta att att cag tta ttt gct act 524
 Gly Arg Arg Val Lys Lys Trp Gln Leu Ile Ile Gln Leu Phe Ala Thr
 10 15 20
 tgt ttt tta gcg agc ctc atg ttt ttt tgg gaa cca atc gat aat cac 572
 Cys Phe Leu Ala Ser Leu Met Phe Phe Trp Glu Pro Ile Asp Asn His
 25 30 35
 att gtg agc cat atg aag tca tat tct tac aga tac ctc ata aat agc 620
 Ile Val Ser His Met Lys Ser Tyr Ser Tyr Arg Tyr Leu Ile Asn Ser
 40 45 50
 tat gac ttt gtg aat gat acc ctg tct ctt aag cac acc tca gcg ggg 668
 Tyr Asp Phe Val Asn Asp Thr Leu Ser Leu Lys His Thr Ser Ala Gly
 55 60 65 70
 cct cgc tac caa tac ttg att aac cac aag gaa aag tgt caa gct caa 716
 Pro Arg Tyr Gln Tyr Leu Ile Asn His Lys Glu Lys Cys Gln Ala Gln
 75 80 85
 gac gtc ctc ctt tta ctg ttt gta aaa act gct cct gaa aac tat gat 764
 Asp Val Leu Leu Leu Phe Val Lys Thr Ala Pro Glu Asn Tyr Asp
 90 95 100
 cga cgt tcc gga att aga agg acg tgg ggc aat gaa aat tat gtt cgg 812
 Arg Arg Ser Gly Ile Arg Arg Thr Trp Gly Asn Glu Asn Tyr Val Arg
 105 110 115
 tct cag ctg aat gcc aac atc aaa act ctg ttt gcc tta gga act cct 860
 Ser Gln Leu Asn Ala Asn Ile Lys Thr Leu Phe Ala Leu Gly Thr Pro
 120 125 130
 aat cca ctg gag gga gaa gaa cta caa aga aaa ctg gct tgg gaa gat 908
 Asn Pro Leu Glu Gly Glu Glu Leu Gln Arg Lys Leu Ala Trp Glu Asp

135	140	145	150	
caa agg tac aat gat	ata att cag caa gac	ttt gtt gat tct ttc tac		956
Gln Arg Tyr Asn Asp	Ile Ile Gln Gln Asp	Phe Val Asp Ser Phe Tyr		
	155	160	165	
aat ctt act ctg aaa tta ctt atg	cag ttc agt tgg gca aat acc tat		1004	
Asn Leu Thr Leu Lys Leu Leu Met	Gln Phe Ser Trp Ala Asn Thr Tyr			
	170	175	180	
tgt cca cat gcc aaa ttt ctt atg	act gct gat gat gac ata ttt att		1052	
Cys Pro His Ala Lys Phe Leu Met	Thr Ala Asp Asp Asp Ile Phe Ile			
	185	190	195	
cac atg cca aat ctg att gag tac	ctt caa agt tta gaa caa att ggt		1100	
His Met Pro Asn Leu Ile Glu Tyr	Leu Gln Ser Leu Glu Gln Ile Gly			
	200	205	210	
gtt caa gac ttt tgg att ggt cgt	gtt cat cgt ggt gcc cct ccc att		1148	
Val Gln Asp Phe Trp Ile Gly Arg	Val His Arg Gly Ala Pro Pro Ile			
	215	220	225	230
aga gat aaa agc agc aaa tac tac	gtg tcc tat gaa atg tac cag tgg		1196	
Arg Asp Lys Ser Ser Lys Tyr Tyr	Val Ser Tyr Glu Met Tyr Gln Trp			
	235	240	245	
cca gct tac cct gac tac aca gcc	gga gct gcc tat gta atc tcc ggt		1244	
Pro Ala Tyr Pro Asp Tyr Thr Ala	Gly Ala Ala Tyr Val Ile Ser Gly			
	250	255	260	
gat gta gct gcc aaa gtc tat gag	gca tca cag aca cta aat tca agt		1292	
Asp Val Ala Ala Lys Val Tyr Glu	Ala Ser Gln Thr Leu Asn Ser Ser			
	265	270	275	
ctt tac ata gac gat gtg ttc atg	ggc ctc tgt gcc aat aaa ata ggg		1340	
Leu Tyr Ile Asp Asp Val Phe Met	Gly Leu Cys Ala Asn Lys Ile Gly			
	280	285	290	
ata gta ccg cag gac cat gtg ttt	ttt tct gga gag ggt aaa act cct		1388	
Ile Val Pro Gln Asp His Val Phe	Phe Ser Gly Glu Gly Lys Thr Pro			
	295	300	305	310
tat cat ccc tgc atc tat gaa aaa	atg atg aca tct cat gga cac tta		1436	
Tyr His Pro Cys Ile Tyr Glu Lys	Met Thr Ser His Gly His Leu			
	315	320	325	
gaa gat ctc cag gac ctt tgg aag	aat gct aca gat cct aaa gta aaa		1484	
Glu Asp Leu Gln Asp Leu Trp Lys	Asn Ala Thr Asp Pro Lys Val Lys			
	330	335	340	
acc att tcc aaa ggt ttt ttt ggt	caa ata tac tgc aga tta atg aag		1532	
Thr Ile Ser Lys Gly Phe Phe Gly	Gln Ile Tyr Cys Arg Leu Met Lys			
	345	350	355	
ata att ctc ctt tgt aaa att agc	tat gtg gac aca tac cct tgt agg		1580	
Ile Ile Leu Leu Cys Lys Ile Ser	Tyr Val Asp Thr Tyr Pro Cys Arg			
	360	365	370	
gct gcg ttt atc taatagtact	tgaatgttgt atgttttcac tgtcactgag		1632	
Ala Ala Phe Ile				
375				

```

tcaaacctgg atgaaaaaaaa cctttaaatg ttcgtctata ccctaagtaa aatgaggacg 1692
aaagacaaat attttgaaag cctagtcctat cagaatgttt ctttgattct agaagctgtt 1752
taatatcact tatctacttc attgcctaag ttcatttcaa agaatttgta tttagaaaag 1812
gtttatatta ttagtgaaaa caaaactaaa gggaagttca agttctcatg taatgccaca 1872
tatatacttg aggtgtagag atgttattaa gaagttttga tgtagaata attgcttttg 1932
gaaaatacca aatgaacgta cagtacaaca tttcaaggaa atgaatatat tgtagacca 1992
ggtaagcaag tttatttttg ttaaagagca cttggtggag gtagtagggg cagggaaagg 2052
tcagcatagg agagaaagtt catgaatctg gtaaaacagt ctcttgttct taagaggaga 2112
tgtagaaaaa tgtgtacaat gttattataa acagacaaat cacgtcttac cacatccatg 2172
tagctactgg tgtagagtc attaaaatac ctttttttgc atcttttttc aaagtttaat 2232
gtgaactttt agaaaagtga ttaatgttgc cctaatactt tatatgtttt taatggattt 2292
ttttttaagt attagaaaat gacacataac acgggcagct ggttgctcat agggtccttc 2352
tctagggaga aaccattggt aattcaaata agctgatttt aatgacgttt tcaactgggt 2412
tttaaatatt caatattggt ctgtgtttaa gtttgttatt tgaatgtaat ttacatagag 2472
gaatataata atggagagac ttcaaatgga aagacagAAC attacaagcc taatgtctcc 2532
ataattttat aaaatgaaat cttagtgtct aaatccttgt actgattact aaaattaacc 2592
cactcctccc caacaaggtc ttataaacca cagcactttg ttccaagttc agagttttaa 2652
attgagagca ttaaacaatca aagtataat atctaaaaca atttattttt catcaataac 2712
tgtcagaggt gatctttatt ttctaataat ttcaaacttg aaaacagagt aaaaaagtga 2772
tagaaaagtt gccagtttgg ggttaaagca tttttaaagc tgcatgttcc ttgtaataca 2832
agagatgtgt ctgagatcta atagagtaag ttacatttat tttaaaagc aggataaaaa 2892
tgtggctata atacacacta cctcccttca ctacagaaag aactagggtg tgctactgct 2952
tagggagatt atatgaaggc caaaataatg acttcagcaa gagtgactga actcactcta 3012
aggcctttga ctgcagaggc acctgttagg gaaaatcaga tgtctcatat aataagggtga 3072
tgtcggaaac acgcaaaaca aaacgaaaaa agatttctca gtatacaca ctgaatgatg 3132
atacttaca ttttttagcag gttagctttt aatgtttaca gaaattttta tttttttcta 3192
ttttgaaatt tgaggcttgt ttacattgct tagataattt agaattttta actaatgtca 3252
aaactacagt gtcaaacatt ctaggttgta gttactttca gagtagatac agggtttttag 3312
atcattacag ttttaagttt ctgaccaatt aaaaaaacat agagaacaaa agcatatttg 3372
accaagcaac aagcttataa ttaattttta ttagttgatt gattaatgat gtattgcctt 3432
ttgcccata ataccctgtg tatctatact tggaagtgtt taagggtgct attggttgaa 3492
aacataagtg tctctggcca tcaaagtgat cttgtttaca gcagtgcctt tgtgaaacaa 3552
ttattttatt gctgaaagag ctcttctgaa ctgtgtcctt ttaatttttg cttagaatag 3612
aatggaacaa gtttaaattt caaggaaata tgaaggcact tccttttttt ctaagaagga 3672
agttgctaga tgattccttc atcacactta cttaaagtac tgagaagagt atctgtaa at 3732
aaaagggttc caacctttta aaaaagaagg aaaaaacttt ttggtgctcc agtgtagggc 3792
tatcttttta aaaaatgtca acaaaggga aataaactat cagcttgat ggtcacttga 3852
atagaagatg gttatacaca gtgttattgt taaaattttt ttaccttttg gttgggttgc 3912
atcttttttc catattgtta attttatacc aaaatgttaa atatttgtat tacttgaatt 3972
ttgctcttgt atggcaaaat aattagttag tttaaaaaaa atctatagtt tccaataaac 4032
aactgaaaaa ttaaaaaaaa 4052

```

<210> 14
 <211> 378
 <212> PRT
 <213> Homo sapiens

```

<400> 14
Met Arg Met Leu Val Ser Gly Arg Arg Val Lys Lys Trp Gln Leu Ile
1          5          10          15
Ile Gln Leu Phe Ala Thr Cys Phe Leu Ala Ser Leu Met Phe Phe Trp
20          25          30
Glu Pro Ile Asp Asn His Ile Val Ser His Met Lys Ser Tyr Ser Tyr
35          40          45
Arg Tyr Leu Ile Asn Ser Tyr Asp Phe Val Asn Asp Thr Leu Ser Leu
50          55          60
Lys His Thr Ser Ala Gly Pro Arg Tyr Gln Tyr Leu Ile Asn His Lys
65          70          75          80
Glu Lys Cys Gln Ala Gln Asp Val Leu Leu Leu Leu Phe Val Lys Thr
85          90          95

```


Ala	Pro	Glu	Asn	Tyr	Asp	Arg	Arg	Ser	Gly	Ile	Arg	Arg	Thr	Trp	Gly	
			100					105					110			
Asn	Glu	Asn	Tyr	Val	Arg	Ser	Gln	Leu	Asn	Ala	Asn	Ile	Lys	Thr	Leu	
		115					120					125				
Phe	Ala	Leu	Gly	Thr	Pro	Asn	Pro	Leu	Glu	Gly	Glu	Glu	Leu	Gln	Arg	
		130				135					140					
Lys	Leu	Ala	Trp	Glu	Asp	Gln	Arg	Tyr	Asn	Asp	Ile	Ile	Gln	Gln	Asp	
145				150						155					160	
Phe	Val	Asp	Ser	Phe	Tyr	Asn	Leu	Thr	Leu	Lys	Leu	Leu	Met	Gln	Phe	
			165					170						175		
Ser	Trp	Ala	Asn	Thr	Tyr	Cys	Pro	His	Ala	Lys	Phe	Leu	Met	Thr	Ala	
		180						185					190			
Asp	Asp	Asp	Ile	Phe	Ile	His	Met	Pro	Asn	Leu	Ile	Glu	Tyr	Leu	Gln	
		195					200					205				
Ser	Leu	Glu	Gln	Ile	Gly	Val	Gln	Asp	Phe	Trp	Ile	Gly	Arg	Val	His	
		210				215					220					
Arg	Gly	Ala	Pro	Pro	Ile	Arg	Asp	Lys	Ser	Ser	Lys	Tyr	Tyr	Val	Ser	
225					230					235					240	
Tyr	Glu	Met	Tyr	Gln	Trp	Pro	Ala	Tyr	Pro	Asp	Tyr	Thr	Ala	Gly	Ala	
				245						250				255		
Ala	Tyr	Val	Ile	Ser	Gly	Asp	Val	Ala	Ala	Lys	Val	Tyr	Glu	Ala	Ser	
			260					265					270			
Gln	Thr	Leu	Asn	Ser	Ser	Leu	Tyr	Ile	Asp	Asp	Val	Phe	Met	Gly	Leu	
		275					280					285				
Cys	Ala	Asn	Lys	Ile	Gly	Ile	Val	Pro	Gln	Asp	His	Val	Phe	Phe	Ser	
		290				295					300					
Gly	Glu	Gly	Lys	Thr	Pro	Tyr	His	Pro	Cys	Ile	Tyr	Glu	Lys	Met	Met	
305					310					315					320	
Thr	Ser	His	Gly	His	Leu	Glu	Asp	Leu	Gln	Asp	Leu	Trp	Lys	Asn	Ala	
				325					330					335		
Thr	Asp	Pro	Lys	Val	Lys	Thr	Ile	Ser	Lys	Gly	Phe	Phe	Gly	Gln	Ile	
			340					345					350			
Tyr	Cys	Arg	Leu	Met	Lys	Ile	Ile	Leu	Leu	Cys	Lys	Ile	Ser	Tyr	Val	
		355				360						365				
Asp	Thr	Tyr	Pro	Cys	Arg	Ala	Ala	Phe	Ile							
		370				375										

<210> 15
 <211> 1134
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1134)

<400> 15																
atg	aga	atg	ttg	gtt	agt	ggc	aga	aga	gtc	aaa	aaa	tgg	cag	tta	att	48
Met	Arg	Met	Leu	Val	Ser	Gly	Arg	Arg	Val	Lys	Lys	Trp	Gln	Leu	Ile	
1				5					10					15		
att	cag	tta	ttt	gct	act	tgt	ttt	tta	gcg	agc	ctc	atg	ttt	ttt	tgg	96
Ile	Gln	Leu	Phe	Ala	Thr	Cys	Phe	Leu	Ala	Ser	Leu	Met	Phe	Phe	Trp	
			20					25					30			
gaa	cca	atc	gat	aat	cac	att	gtg	agc	cat	atg	aag	tca	tat	tct	tac	144
Glu	Pro	Ile	Asp	Asn	His	Ile	Val	Ser	His	Met	Lys	Ser	Tyr	Ser	Tyr	
		35					40					45				
aga	tac	ctc	ata	aat	agc	tat	gac	ttt	gtg	aat	gat	acc	ctg	tct	ctt	192

Arg	Tyr	Leu	Ile	Asn	Ser	Tyr	Asp	Phe	Val	Asn	Asp	Thr	Leu	Ser	Leu		
	50					55					60						
aag	cac	acc	tca	gcg	ggg	cct	cgc	tac	caa	tac	ttg	att	aac	cac	aag	240	
Lys	His	Thr	Ser	Ala	Gly	Pro	Arg	Tyr	Gln	Tyr	Leu	Ile	Asn	His	Lys		
	65				70					75					80		
gaa	aag	tgt	caa	gct	caa	gac	gtc	ctc	ctt	tta	ctg	ttt	gta	aaa	act	288	
Glu	Lys	Cys	Gln	Ala	Gln	Asp	Val	Leu	Leu	Leu	Leu	Phe	Val	Lys	Thr		
				85				90						95			
gct	cct	gaa	aac	tat	gat	cga	cgt	tcc	gga	att	aga	agg	acg	tgg	ggc	336	
Ala	Pro	Glu	Asn	Tyr	Asp	Arg	Arg	Ser	Gly	Ile	Arg	Arg	Thr	Trp	Gly		
			100					105					110				
aat	gaa	aat	tat	gtt	cgg	tct	cag	ctg	aat	gcc	aac	atc	aaa	act	ctg	384	
Asn	Glu	Asn	Tyr	Val	Arg	Ser	Gln	Leu	Asn	Ala	Asn	Ile	Lys	Thr	Leu		
		115					120					125					
ttt	gcc	tta	gga	act	cct	aat	cca	ctg	gag	gga	gaa	gaa	cta	caa	aga	432	
Phe	Ala	Leu	Gly	Thr	Pro	Asn	Pro	Leu	Glu	Gly	Glu	Glu	Leu	Gln	Arg		
	130					135					140						
aaa	ctg	gct	tgg	gaa	gat	caa	agg	tac	aat	gat	ata	att	cag	caa	gac	480	
Lys	Leu	Ala	Trp	Glu	Asp	Gln	Arg	Tyr	Asn	Asp	Ile	Ile	Gln	Gln	Asp		
	145				150					155					160		
ttt	gtt	gat	tct	ttc	tac	aat	ctt	act	ctg	aaa	tta	ctt	atg	cag	ttc	528	
Phe	Val	Asp	Ser	Phe	Tyr	Asn	Leu	Thr	Leu	Lys	Leu	Leu	Met	Gln	Phe		
				165				170						175			
agt	tgg	gca	aat	acc	tat	tgt	cca	cat	gcc	aaa	ttt	ctt	atg	act	gct	576	
Ser	Trp	Ala	Asn	Thr	Tyr	Cys	Pro	His	Ala	Lys	Phe	Leu	Met	Thr	Ala		
			180					185					190				
gat	gat	gac	ata	ttt	att	cac	atg	cca	aat	ctg	att	gag	tac	ctt	caa	624	
Asp	Asp	Asp	Ile	Phe	Ile	His	Met	Pro	Asn	Leu	Ile	Glu	Tyr	Leu	Gln		
		195					200					205					
agt	tta	gaa	caa	att	ggg	gtt	caa	gac	ttt	tgg	att	ggg	cgt	gtt	cat	672	
Ser	Leu	Glu	Gln	Ile	Gly	Val	Gln	Asp	Phe	Trp	Ile	Gly	Arg	Val	His		
	210					215					220						
cgt	ggg	gcc	cct	ccc	att	aga	gat	aaa	agc	agc	aaa	tac	tac	gtg	tcc	720	
Arg	Gly	Ala	Pro	Pro	Ile	Arg	Asp	Lys	Ser	Ser	Lys	Tyr	Tyr	Val	Ser		
	225				230					235					240		
tat	gaa	atg	tac	cag	tgg	cca	gct	tac	cct	gac	tac	aca	gcc	gga	gct	768	
Tyr	Glu	Met	Tyr	Gln	Trp	Pro	Ala	Tyr	Pro	Asp	Tyr	Thr	Ala	Gly	Ala		
				245					250					255			
gcc	tat	gta	atc	tcc	ggg	gat	gta	gct	gcc	aaa	gtc	tat	gag	gca	tca	816	
Ala	Tyr	Val	Ile	Ser	Gly	Asp	Val	Ala	Ala	Lys	Val	Tyr	Glu	Ala	Ser		
			260					265					270				
cag	aca	cta	aat	tca	agt	ctt	tac	ata	gac	gat	gtg	ttc	atg	ggc	ctc	864	
Gln	Thr	Leu	Asn	Ser	Ser	Leu	Tyr	Ile	Asp	Asp	Val	Phe	Met	Gly	Leu		
		275					280					285					
tgt	gcc	aat	aaa	ata	ggg	ata	gta	ccg	cag	gac	cat	gtg	ttt	ttt	tct	912	
Cys	Ala	Asn	Lys	Ile	Gly	Ile	Val	Pro	Gln	Asp	His	Val	Phe	Phe	Ser		

290	295	300	
gga gag ggt aaa act cct tat cat ccc tgc atc tat gaa aaa atg atg			960
Gly Glu Gly Lys Thr Pro Tyr His Pro Cys Ile Tyr Glu Lys Met Met			
305	310	315	320
aca tct cat gga cac tta gaa gat ctc cag gac ctt tgg aag aat gct			1008
Thr Ser His Gly His Leu Glu Asp Leu Gln Asp Leu Trp Lys Asn Ala			
	325	330	335
aca gat cct aaa gta aaa acc att tcc aaa ggt ttt ttt ggt caa ata			1056
Thr Asp Pro Lys Val Lys Thr Ile Ser Lys Gly Phe Phe Gly Gln Ile			
	340	345	350
tac tgc aga tta atg aag ata att ctc ctt tgt aaa att agc tat gtg			1104
Tyr Cys Arg Leu Met Lys Ile Ile Leu Leu Cys Lys Ile Ser Tyr Val			
	355	360	365
gac aca tac cct tgt agg gct gcg ttt atc			1134
Asp Thr Tyr Pro Cys Arg Ala Ala Phe Ile			
370	375		
<210> 16			
<211> 1976			
<212> DNA			
<213> Homo sapiens			
<220>			
<221> CDS			
<222> (1)...(1614)			
<221> misc_feature			
<222> (1)...(1976)			
<223> n = A, T, C or G			
<400> 16			
atg gcc ctg ctg gcg cgg atc ctg aga gcc ggg ctg cgg ccg gcg ccc			48
Met Ala Leu Leu Ala Arg Ile Leu Arg Ala Gly Leu Arg Pro Ala Pro			
1	5	10	15
gag cgg ggt ggg ctc ctg ggc ggc ggg gcc ccg cgg cgg cct caa ccc			96
Glu Arg Gly Gly Leu Leu Gly Gly Gly Ala Pro Arg Arg Pro Gln Pro			
	20	25	30
gcg ggc gca cgg ctc ccg gcg ggg gcg cgg gcc gag gac aaa ggc gcc			144
Ala Gly Ala Arg Leu Pro Ala Gly Ala Arg Ala Glu Asp Lys Gly Ala			
	35	40	45
ggg cgg ccg ggg tcg ccg ccg gga ggg ggc cga gcc gag ggt ccc cgg			192
Gly Arg Pro Gly Ser Pro Pro Gly Gly Gly Arg Ala Glu Gly Pro Arg			
	50	55	60
agc ctc gcc gcc atg ccg ggg ccg agg acc ctc gcc aac ctg gcg gag			240
Ser Leu Ala Ala Met Pro Gly Pro Arg Thr Leu Ala Asn Leu Ala Glu			
65	70	75	80
ttc ttc tgc agg gac ggc ttc agc cgc atc cac gag atc cag cag aag			288
Phe Phe Cys Arg Asp Gly Phe Ser Arg Ile His Glu Ile Gln Gln Lys			
	85	90	95

cac	aca	cgg	gaa	tat	gga	aaa	atc	ttc	aag	tct	cac	ttt	ggt	cct	cag	336
His	Thr	Arg	Glu	Tyr	Gly	Lys	Ile	Phe	Lys	Ser	His	Phe	Gly	Pro	Gln	
			100					105					110			
ttt	gta	gta	tct	att	gca	gac	cgc	gat	atg	gtg	gct	cag	gtg	ctc	cgg	384
Phe	Val	Val	Ser	Ile	Ala	Asp	Arg	Asp	Met	Val	Ala	Gln	Val	Leu	Arg	
			115				120					125				
gcg	gag	ggc	gct	gcg	ccc	cag	aga	gcc	aac	atg	gag	tcc	tgg	cgg	gag	432
Ala	Glu	Gly	Ala	Ala	Pro	Gln	Arg	Ala	Asn	Met	Glu	Ser	Trp	Arg	Glu	
	130					135					140					
tac	cga	gac	ttg	cgg	ggg	aga	gcc	acc	ggg	ctc	atc	tcg	gcg	gag	ggt	480
Tyr	Arg	Asp	Leu	Arg	Gly	Arg	Ala	Thr	Gly	Leu	Ile	Ser	Ala	Glu	Gly	
145					150					155					160	
gaa	cag	tgg	ctc	aag	atg	aga	agc	gta	ttg	aga	caa	aga	att	ctg	aaa	528
Glu	Gln	Trp	Leu	Lys	Met	Arg	Ser	Val	Leu	Arg	Gln	Arg	Ile	Leu	Lys	
				165					170					175		
ccg	aaa	gat	gtg	gcc	att	tat	tct	gga	gaa	gtc	gac	caa	gtt	att	gct	576
Pro	Lys	Asp	Val	Ala	Ile	Tyr	Ser	Gly	Glu	Val	Asp	Gln	Val	Ile	Ala	
			180					185					190			
gac	tta	att	aaa	aga	atc	tac	ctc	ctc	agg	agc	cag	gca	gaa	gat	gga	624
Asp	Leu	Ile	Lys	Arg	Ile	Tyr	Leu	Leu	Arg	Ser	Gln	Ala	Glu	Asp	Gly	
			195				200					205				
gaa	acc	gtg	acc	aat	gtc	aat	gat	ctt	ttc	ttc	aaa	tat	tca	atg	gaa	672
Glu	Thr	Val	Thr	Asn	Val	Asn	Asp	Leu	Phe	Phe	Lys	Tyr	Ser	Met	Glu	
	210					215					220					
gga	gtg	gcc	acc	atc	ctt	tat	gag	agt	cgt	ttg	ggc	tgc	ctg	gaa	aac	720
Gly	Val	Ala	Thr	Ile	Leu	Tyr	Glu	Ser	Arg	Leu	Gly	Cys	Leu	Glu	Asn	
225					230					235					240	
agc	atc	cca	cag	ctg	act	gtg	gaa	tac	atc	gag	gcc	ctg	gag	ctc	atg	768
Ser	Ile	Pro	Gln	Leu	Thr	Val	Glu	Tyr	Ile	Glu	Ala	Leu	Glu	Leu	Met	
				245					250					255		
ttt	agc	atg	ttc	aag	acc	tcc	atg	tat	gca	ggc	gcc	atc	ccc	aga	tgg	816
Phe	Ser	Met	Phe	Lys	Thr	Ser	Met	Tyr	Ala	Gly	Ala	Ile	Pro	Arg	Trp	
			260					265					270			
ctt	cgc	ccc	ttc	atc	cca	aag	ccc	tgg	cgg	gaa	ttc	tgc	agg	tcc	tgg	864
Leu	Arg	Pro	Phe	Ile	Pro	Lys	Pro	Trp	Arg	Glu	Phe	Cys	Arg	Ser	Trp	
			275				280					285				
gat	gga	ctc	ttc	aaa	ttc	agc	caa	att	cat	gtt	gac	aac	aag	ttg	tgg	912
Asp	Gly	Leu	Phe	Lys	Phe	Ser	Gln	Ile	His	Val	Asp	Asn	Lys	Leu	Trp	
	290					295					300					
gac	ata	cag	tac	caa	atg	gac	cga	ggc	cgg	agg	gtg	agc	ggg	gga	ctt	960
Asp	Ile	Gln	Tyr	Gln	Met	Asp	Arg	Gly	Arg	Arg	Val	Ser	Gly	Gly	Leu	
305					310					315					320	
ctc	aca	tac	ctc	ttc	ctt	agc	cag	gct	ctg	acg	ctg	cag	gag	atc	tac	1008
Leu	Thr	Tyr	Leu	Phe	Leu	Ser	Gln	Ala	Leu	Thr	Leu	Gln	Glu	Ile	Tyr	
				325					330					335		
gcc	aac	gtg	act	gag	atg	ctg	ctg	gcc	ggc	gtc	gac	acg	acg	tcc	ttc	1056

Ala Asn Val Thr Glu Met Leu Leu Ala Gly Val Asp Thr Thr Ser Phe	
340 345 350	
acc ttg tct tgg acg gtg tac ctc ctg gca agg cac cca gaa gtg cag	1104
Thr Leu Ser Trp Thr Val Tyr Leu Leu Ala Arg His Pro Glu Val Gln	
355 360 365	
cag acg gtg tac cgg gag att gtg aag aat tta ggg gaa agg cat gtt	1152
Gln Thr Val Tyr Arg Glu Ile Val Lys Asn Leu Gly Glu Arg His Val	
370 375 380	
cca act gca gct gat gtc ccc aag gtc ccg ctg gtc aga gct ctc ctt	1200
Pro Thr Ala Ala Asp Val Pro Lys Val Pro Leu Val Arg Ala Leu Leu	
385 390 395 400	
aag gaa acc ctg agg ctg ttt cca gtg ctg cca ggg aac ggc cgg gtc	1248
Lys Glu Thr Leu Arg Leu Phe Pro Val Leu Pro Gly Asn Gly Arg Val	
405 410 415	
acc cag gaa gac ctg gtt att ggc ggg tat ctg att ccg aaa ggc acc	1296
Thr Gln Glu Asp Leu Val Ile Gly Gly Tyr Leu Ile Pro Lys Gly Thr	
420 425 430	
cag ctg gcc ctt tgc cac tat gcc aca tcg cac cag gat gag aac ttc	1344
Gln Leu Ala Leu Cys His Tyr Ala Thr Ser His Gln Asp Glu Asn Phe	
435 440 445	
cct cgg gcc aag gag ttc cga cct gag cgc tgg ctg cgg aaa gga gac	1392
Pro Arg Ala Lys Glu Phe Arg Pro Glu Arg Trp Leu Arg Lys Gly Asp	
450 455 460	
tta gat aga gtt gac aat ttt gga tcc atc ccc ttt ggt cat ggg gtt	1440
Leu Asp Arg Val Asp Asn Phe Gly Ser Ile Pro Phe Gly His Gly Val	
465 470 475 480	
cgc agc tgc ata ggg cgg aga att gca gaa ctg gag att cac ctc gtc	1488
Arg Ser Cys Ile Gly Arg Arg Ile Ala Glu Leu Glu Ile His Leu Val	
485 490 495	
gtg atc cag ttg ctt caa cat ttt gag atc aaa aca tct tct cag acc	1536
Val Ile Gln Leu Leu Gln His Phe Glu Ile Lys Thr Ser Ser Gln Thr	
500 505 510	
aat gct gtt cat gca aaa acc cac ggg ctc ctg acg cca ggg ggg ccc	1584
Asn Ala Val His Ala Lys Thr His Gly Leu Leu Thr Pro Gly Gly Pro	
515 520 525	
atc cac gtg cga ttt gtt aac aga aag taa gcctagattt taaacctggg	1634
Ile His Val Arg Phe Val Asn Arg Lys *	
530 535	
ctgatgtagc agaccagctc gccgacacac agtgggtatt tgtgttcgct gatcaccgtg	1694
gagaaggaaa gcgatgtcgc taaaggctgt cttgttatag actggcctcc caggtcctgg	1754
gacacttgta aatctttatg caaagtaatg taaaaagggtt gctattttac tgggtgcatc	1814
cagaagttgc cctttctttg ggggaaacag ctgttttaaaa accagtggca gtgaattttt	1874
atgcttcata cattgngcta gactcaatat ttaatgactg gcagtatcct gtgcatttac	1934
ttgtacaggg aaatggtggn ttactttacaa attcagttct tc	1976

<210> 17
 <211> 537
 <212> PRT

<400> 17

30

Leu Asp Arg Val Asp Asn Phe Gly Ser Ile Pro Phe Gly His Gly Val
 465 470 475 480
 Arg Ser Cys Ile Gly Arg Arg Ile Ala Glu Leu Glu Ile His Leu Val
 485 490 495
 Val Ile Gln Leu Leu Gln His Phe Glu Ile Lys Thr Ser Ser Gln Thr
 500 505 510
 Asn Ala Val His Ala Lys Thr His Gly Leu Leu Thr Pro Gly Gly Pro
 515 520 525
 Ile His Val Arg Phe Val Asn Arg Lys
 530 535

<210> 18
 <211> 1614
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1614)

<400> 18
 atg gcc ctg ctg gcg cgg atc ctg aga gcc ggg ctg cgg ccg gcg ccc 48
 Met Ala Leu Leu Ala Arg Ile Leu Arg Ala Gly Leu Arg Pro Ala Pro
 1 5 10 15
 gag cgg ggt ggg ctc ctg ggc ggc ggg gcc ccg cgg cgg cct caa ccc 96
 Glu Arg Gly Gly Leu Leu Gly Gly Gly Ala Pro Arg Arg Pro Gln Pro
 20 25 30
 gcg ggc gca cgg ctc ccg gcg ggg gcg cgg gcc gag gac aaa ggc gcc 144
 Ala Gly Ala Arg Leu Pro Ala Gly Ala Arg Ala Glu Asp Lys Gly Ala
 35 40 45
 ggg cgg ccg ggg tcg ccg ccg gga ggg ggc cga gcc gag ggt ccc cgg 192
 Gly Arg Pro Gly Ser Pro Pro Gly Gly Gly Arg Ala Glu Gly Pro Arg
 50 55 60
 agc ctc gcc gcc atg ccg ggg ccg agg acc ctc gcc aac ctg gcg gag 240
 Ser Leu Ala Ala Met Pro Gly Pro Arg Thr Leu Ala Asn Leu Ala Glu
 65 70 75 80
 ttc ttc tgc agg gac ggc ttc agc cgc atc cac gag atc cag cag aag 288
 Phe Phe Cys Arg Asp Gly Phe Ser Arg Ile His Glu Ile Gln Gln Lys
 85 90 95
 cac aca cgg gaa tat gga aaa atc ttc aag tct cac ttt ggt cct cag 336
 His Thr Arg Glu Tyr Gly Lys Ile Phe Lys Ser His Phe Gly Pro Gln
 100 105 110
 ttt gta gta tct att gca gac cgc gat atg gtg gct cag gtg ctc cgg 384
 Phe Val Val Ser Ile Ala Asp Arg Asp Met Val Ala Gln Val Leu Arg
 115 120 125
 gcg gag ggc gct gcg ccc cag aga gcc aac atg gag tcc tgg cgg gag 432
 Ala Glu Gly Ala Ala Pro Gln Arg Ala Asn Met Glu Ser Trp Arg Glu
 130 135 140
 tac cga gac ttg cgg ggg aga gcc acc ggg ctc atc tcg gcg gag ggt 480
 Tyr Arg Asp Leu Arg Gly Arg Ala Thr Gly Leu Ile Ser Ala Glu Gly
 145 150 155 160

gaa cag tgg ctc aag atg aga agc gta ttg aga caa aga att ctg aaa	528
Glu Gln Trp Leu Lys Met Arg Ser Val Leu Arg Gln Arg Ile Leu Lys	
165 170 175	
ccg aaa gat gtg gcc att tat tct gga gaa gtc gac caa gtt att gct	576
Pro Lys Asp Val Ala Ile Tyr Ser Gly Glu Val Asp Gln Val Ile Ala	
180 185 190	
gac tta att aaa aga atc tac ctc ctc agg agc cag gca gaa gat gga	624
Asp Leu Ile Lys Arg Ile Tyr Leu Leu Arg Ser Gln Ala Glu Asp Gly	
195 200 205	
gaa acc gtg acc aat gtc aat gat ctt ttc ttc aaa tat tca atg gaa	672
Glu Thr Val Thr Asn Val Asn Asp Leu Phe Phe Lys Tyr Ser Met Glu	
210 215 220	
gga gtg gcc acc atc ctt tat gag agt cgt ttg ggc tgc ctg gaa aac	720
Gly Val Ala Thr Ile Leu Tyr Glu Ser Arg Leu Gly Cys Leu Glu Asn	
225 230 235 240	
agc atc cca cag ctg act gtg gaa tac atc gag gcc ctg gag ctc atg	768
Ser Ile Pro Gln Leu Thr Val Glu Tyr Ile Glu Ala Leu Glu Leu Met	
245 250 255	
ttt agc atg ttc aag acc tcc atg tat gca ggc gcc atc ccc aga tgg	816
Phe Ser Met Phe Lys Thr Ser Met Tyr Ala Gly Ala Ile Pro Arg Trp	
260 265 270	
ctt cgc ccc ttc atc cca aag ccc tgg cgg gaa ttc tgc agg tcc tgg	864
Leu Arg Pro Phe Ile Pro Lys Pro Trp Arg Glu Phe Cys Arg Ser Trp	
275 280 285	
gat gga ctc ttc aaa ttc agc caa att cat gtt gac aac aag ttg tgg	912
Asp Gly Leu Phe Lys Phe Ser Gln Ile His Val Asp Asn Lys Leu Trp	
290 295 300	
gac ata cag tac caa atg gac cga ggc cgg agg gtg agc ggg gga ctt	960
Asp Ile Gln Tyr Gln Met Asp Arg Gly Arg Arg Val Ser Gly Gly Leu	
305 310 315 320	
ctc aca tac ctc ttc ctt agc cag gct ctg acg ctg cag gag atc tac	1008
Leu Thr Tyr Leu Phe Leu Ser Gln Ala Leu Thr Leu Gln Glu Ile Tyr	
325 330 335	
gcc aac gtg act gag atg ctg ctg gcc ggc gtc gac acg acg tcc ttc	1056
Ala Asn Val Thr Glu Met Leu Leu Ala Gly Val Asp Thr Thr Ser Phe	
340 345 350	
acc ttg tct tgg acg gtg tac ctc ctg gca agg cac cca gaa gtg cag	1104
Thr Leu Ser Trp Thr Val Tyr Leu Leu Ala Arg His Pro Glu Val Gln	
355 360 365	
cag acg gtg tac cgg gag att gtg aag aat tta ggg gaa agg cat gtt	1152
Gln Thr Val Tyr Arg Glu Ile Val Lys Asn Leu Gly Glu Arg His Val	
370 375 380	
cca act gca gct gat gtc ccc aag gtc ccg ctg gtc aga gct ctc ctt	1200
Pro Thr Ala Ala Asp Val Pro Lys Val Pro Leu Val Arg Ala Leu Leu	
385 390 395 400	

aag gaa acc ctg agg ctg ttt cca gtg ctg cca ggg aac ggc cgg gtc	1248
Lys Glu Thr Leu Arg Leu Phe Pro Val Leu Pro Gly Asn Gly Arg Val	
405 410 415	
acc cag gaa gac ctg gtt att ggc ggg tat ctg att ccg aaa ggc acc	1296
Thr Gln Glu Asp Leu Val Ile Gly Gly Tyr Leu Ile Pro Lys Gly Thr	
420 425 430	
cag ctg gcc ctt tgc cac tat gcc aca tcg cac cag gat gag aac ttc	1344
Gln Leu Ala Leu Cys His Tyr Ala Thr Ser His Gln Asp Glu Asn Phe	
435 440 445	
cct cgg gcc aag gag ttc cga cct gag cgc tgg ctg cgg aaa gga gac	1392
Pro Arg Ala Lys Glu Phe Arg Pro Glu Arg Trp Leu Arg Lys Gly Asp	
450 455 460	
tta gat aga gtt gac aat ttt gga tcc atc ccc ttt ggt cat ggg gtt	1440
Leu Asp Arg Val Asp Asn Phe Gly Ser Ile Pro Phe Gly His Gly Val	
465 470 475 480	
cgc agc tgc ata ggg cgg aga att gca gaa ctg gag att cac ctc gtc	1488
Arg Ser Cys Ile Gly Arg Arg Ile Ala Glu Leu Glu Ile His Leu Val	
485 490 495	
gtg atc cag ttg ctt caa cat ttt gag atc aaa aca tct tct cag acc	1536
Val Ile Gln Leu Gln His Phe Glu Ile Lys Thr Ser Ser Gln Thr	
500 505 510	
aat gct gtt cat gca aaa acc cac ggg ctc ctg acg cca ggg ggg ccc	1584
Asn Ala Val His Ala Lys Thr His Gly Leu Leu Thr Pro Gly Gly Pro	
515 520 525	
atc cac gtg cga ttt gtt aac aga aag taa	1614
Ile His Val Arg Phe Val Asn Arg Lys *	
530 535	

<210> 19

<211> 496

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 19

Pro Pro Gly Pro Pro Pro Leu Pro Leu Ile Gly Asn Leu Leu Gln Leu	
1 5 10 15	
Gly Arg Ala Pro Gly Pro Ile Pro His Ser Leu Thr Lys Leu Arg Lys	
20 25 30	
Ala Lys Arg Tyr Gly Lys Pro Val Phe Thr Leu Tyr Leu Gly Pro Arg	
35 40 45	
Pro Val Val Val Leu Thr Gly Pro Glu Ala Val Lys Glu Val Leu Ile	
50 55 60	
Asp Lys Gly Glu Glu Phe Ala Lys Gly Arg Gly Asp Phe Asn Pro Thr	
65 70 75 80	
Phe Pro Trp Leu Ser Lys Gly Tyr Arg Glu Gln Gly Leu Leu Phe Ser	
85 90 95	
Asp Asn Gly Pro Lys Trp Arg Lys Leu Arg Arg Phe Ser Leu Leu Thr	
100 105 110	
Leu Arg Phe His Phe Gly Met Gly Ala Tyr Ser Lys Arg Ser Gln Lys	

				245					250					255			
Arg	Leu	Gln	Ala	Ala	Asp	Val	Pro	Gly	Asp	Met	Ile	Lys	Arg	Ile	Phe		
			260						265				270				
Val	Asp	Leu	Val	Ile	Ala	Ala	Gly	Asp	Thr	Thr	Ala	Phe	Ser	Ser	Gln		
		275						280				285					
Trp	Ala	Leu	Phe	Ala	Leu	Ser	Lys	Glu	Pro	Arg	Leu	Gln	Gln	Arg	Leu		
	290					295					300						
Ala	Lys	Glu	Arg	Ala	Thr	Asn	Asp	Ser	Arg	Leu	Met	His	Gly	Leu	Ile		
305					310					315					320		
Lys	Glu	Ser	Leu	Arg	Leu	Tyr											
				325													

<210> 22
 <211> 87
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Consensus amino acid sequence

<400> 22																	
Leu	Ala	Asp	Ile	Pro	Gly	Pro	Gly	Thr	Leu	Arg	Phe	Leu	Phe	Gln	Leu		
1				5					10					15			
Phe	Cys	Lys	Gly	Tyr	Leu	Leu	His	Leu	His	Glu	Leu	Gln	Val	Leu	Gly		
			20					25					30				
Lys	Ala	Arg	Tyr	Gly	Pro	Met	Trp	Met	Ser	Ser	Phe	Gly	Thr	Gln	Arg		
		35					40					45					
Thr	Val	Asn	Leu	Ala	Ser	Pro	Pro	Leu	Val	Glu	Gln	Val	Met	Arg	Gln		
	50					55					60						
Glu	Gly	Lys	Tyr	Pro	Val	Arg	Cys	Ser	Phe	Glu	Pro	Trp	Lys	Glu	His		
65					70					75					80		
Arg	Arg	Arg	His	Gln	Arg	Ala											
				85													

<210> 23
 <211> 82
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Consensus amino acid sequence

<400> 23																	
Asp	Leu	Gln	Lys	Leu	Pro	Tyr	Leu	Asp	Ala	Val	Ile	Lys	Glu	Thr	Leu		
1				5					10					15			
Arg	Leu	His	Pro	Pro	Val	Pro	Thr	Val	Met	Arg	Lys	Val	Lys	Lys	Asp		
			20					25					30				
Met	Glu	Val	Ser	Gly	Thr	Val	Gly	Gly	Glu	Tyr	Thr	Ile	Pro	Lys	Gly		
		35					40					45					
Thr	Gln	Val	Met	Val	Ser	Pro	Tyr	Val	Met	Thr	His	Arg	Asp	Pro	Glu		
	50					55					60						
Tyr	Tyr	Pro	Asp	Pro	Glu	Glu	Phe	Asn	Pro	Glu	Arg	Trp	Leu	Glu	Pro		
65					70					75					80		
Ser	Glu																

<210> 24
 <211> 319

<212> PRT
 <213> Artificial Sequence

<220>
 <223> Consensus amino acid sequence

<400> 24
 Lys Gln Tyr Gly Pro Ile Phe Arg Phe Gln Met Gly Arg Gln Pro Leu
 1 5 10 15
 Ile Ile Ile Ala Glu Ala Glu Leu Cys Arg Glu Val Gly Ile Lys Lys
 20 25 30
 Phe Lys Asp Leu Pro Asn Arg Ser Ile Pro Ser Pro Ile Ser Ala Ser
 35 40 45
 Pro Leu His Lys Lys Gly Leu Phe Phe Thr Arg Asp Lys Arg Trp Ser
 50 55 60
 Lys Met Arg Asn Thr Ile Leu Ser Leu Tyr Gln Pro Ser His Leu Thr
 65 70 75 80
 Ser Leu Ile Pro Thr Met His Ser Phe Ile Thr Ser Ala Thr His Asn
 85 90 95
 Leu Asp Ser Lys Pro Arg Asp Ile Val Phe Ser Asn Leu Phe Leu Lys
 100 105 110
 Leu Thr Thr Asp Ile Ile Gly Gln Ala Ala Phe Gly Val Asp Phe Gly
 115 120 125
 Leu Ser Gly Lys Lys Pro Ile Lys Asp Val Glu Val Thr Asp Phe Ile
 130 135 140
 Asn Gln His Val Tyr Ser Thr Thr Gln Leu Lys Met Asp Leu Ser Gly
 145 150 155 160
 Ser Leu Ser Ile Ile Leu Gly Leu Leu Ile Pro Ile Leu Gln Glu Pro
 165 170 175
 Phe Arg Gln Val Leu Lys Arg Ile Pro Gly Thr Met Asp Trp Arg Val
 180 185 190
 Glu Lys Thr Asn Ala Arg Leu Ser Gly Gln Leu Asn Glu Ile Val Ser
 195 200 205
 Lys Arg Ala Lys Glu Ala Glu Thr Asp Ser Lys Asp Phe Leu Ser Leu
 210 215 220
 Ile Leu Lys Ala Arg Glu Ser Asp Pro Phe Ala Lys Asn Ile Phe Thr
 225 230 235 240
 Ser Asp Tyr Ile Ser Ala Val Thr Tyr Glu His Leu Leu Ala Gly Ser
 245 250 255
 Ala Thr Thr Ala Phe Thr Leu Ser Ser Val Leu Tyr Leu Val Ser Gly
 260 265 270
 His Leu Asp Val Glu Lys Arg Leu Leu Gln Glu Ile Asp Gly Phe Gly
 275 280 285
 Asn Arg Asp Leu Ile Pro Thr Ala His Asp Leu Gln His Lys Phe Pro
 290 295 300
 Tyr Leu Asp Gln Val Ile Lys Glu Ala Met Arg Phe Tyr Met Val
 305 310 315

<210> 25
 <211> 138
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Consensus amino acid sequence

<400> 25
 Ala Ile Pro Gly Pro Arg Gly Pro Phe Gly Met Gly Asn Leu Tyr Asn
 1 5 10 15
 Tyr Leu Pro Gly Ile Gly Ser Tyr Ser Trp Leu Arg Leu His Gln Ala

	275		280		285
Asn	Ala	Phe	Leu	Phe	Glu
Val	Val	Arg	Met	Tyr	Pro
Pro	Pro	Leu			
290		295		300	

<210> 27
 <211> 138
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Consensus amino acid sequence

<400> 27
 Leu Arg Gln Val Gln Asp Glu Thr Ile Arg Leu Ser Thr Leu Ala Pro
 1 5 10 15
 Trp Ala Ala Arg Tyr Ser Asp Lys Lys Val Thr Val Cys Gly Tyr Thr
 20 25 30
 Ile Pro Ala Lys Thr Pro Met Ile His Ala Leu Gly Val Gly Leu Lys
 35 40 45
 Asn Lys Thr Val Trp Glu Asn Thr Asp Ser Trp Asp Pro Asp Arg Phe
 50 55 60
 Ser Pro Asn Gly Arg Arg Gly Asn Asp Phe Cys Pro Phe Gly Val His
 65 70 75 80
 Ser Arg Arg Lys Cys Pro Gly Tyr Leu Phe Ser Tyr Phe Glu Val Gly
 85 90 95
 Val Phe Ala Ser Ile Leu Leu Ser Arg Phe Glu Ile Val Pro Val Glu
 100 105 110
 Gly Gln Thr Val Ile Gln Val His Gly Leu Val Thr Glu Pro Lys Asp
 115 120 125
 Asp Ile Lys Ile Tyr Ile Arg Ser Arg Lys
 130 135

<210> 28
 <211> 67
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Consensus amino acid sequence

<400> 28
 Ile Ala Gly Met Asp Thr Ala Ala Asn Ser Leu Ala Phe Val Leu Tyr
 1 5 10 15
 Arg Met His Leu His Ser Glu Phe Leu Pro Ala Leu Arg Ala Glu Ala
 20 25 30
 Asp Ala Leu Phe Arg Asp Gly Pro Pro Thr Ala Glu Ala Leu Gly Arg
 35 40 45
 Ser Pro Leu Leu His Arg Phe Val Met Glu Thr Leu Arg Val His Pro
 50 55 60
 Ile Ala Pro
 65

<210> 29
 <211> 95
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 29

Val	Pro	Ala	Pro	Pro	Phe	Leu	Gly	His	Ala	Ala	Glu	Met	Gly	Thr	Ile
1				5					10					15	
Lys	Leu	Arg	Pro	Phe	Leu	Thr	Arg	Cys	Tyr	Gln	Ala	Tyr	Gly	Pro	Val
			20					25					30		
Phe	Gln	Leu	Thr	Val	Pro	Gly	Gln	Lys	Ile	Thr	Val	Leu	Ala	Gly	Pro
		35					40					45			
Glu	Ala	Asn	Leu	Phe	Ala	Met	Lys	Glu	Gly	His	Arg	Val	Leu	Arg	Ser
	50					55					60				
Leu	Glu	Ala	Trp	Arg	Asp	Asn	Asp	His	Glu	Met	Gly	Ser	Asp	Arg	Ser
65					70					75					80
Met	Ile	Ser	Leu	Asp	Gly	Ala	Glu	His	Arg	Ala	Tyr	Arg	Arg	Val	
				85					90					95	

<210> 30

<211> 131

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 30

Thr	Val	Ala	Ile	Ser	Pro	Tyr	Gly	Glu	Gln	Trp	Lys	Lys	Met	Arg	Lys
1				5					10					15	
Val	Ile	Thr	Thr	Glu	Ile	Met	Ser	Pro	Lys	Arg	Leu	Asn	Trp	Leu	Leu
			20					25					30		
Gly	Lys	Arg	Thr	Glu	Glu	Ala	Asp	Asn	Leu	Val	Ala	Tyr	Val	His	Asn
		35					40					45			
Met	Cys	Gln	Lys	Ser	Glu	Thr	Asn	Asn	Lys	His	Gly	Ala	Val	Ile	Asp
	50					55					60				
Val	Arg	Asp	Val	Val	Arg	His	Tyr	Cys	His	Asn	Val	Val	Met	Arg	Met
65					70					75					80
Met	Phe	Gly	Arg	Arg	His	Phe	Gly	Lys	Gly	Thr	Glx	Phe	Ser	Asp	Asp
				85					90					95	
Gly	Gly	Pro	Gly	Pro	Glu	Glu	Lys	Glu	His	Met	Asp	Ala	Ile	Phe	Thr
		100						105					110		
Ala	Leu	Asp	Cys	Leu	Tyr	Ala	Phe	Cys	Val	Ser	Asp	Tyr	Ile	Pro	Arg
		115					120					125			
Trp	Leu	Arg													
	130														

<210> 31

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 31

Arg	Trp	Leu	Arg	Gly	Trp	Asp	Leu	Asp
1				5				

<210> 32

<211> 1772

<212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (169)...(1242)

<221> misc_feature
 <222> (1)...(1772)
 <223> n = A, T, C or G

```

<400> 32
ncngnncgcg gcggcgtgcg cagcagcgaa agaggaaact gcagaggagg aagctgcgcc 60
gcagcccgag ccgccccgca tccccgccgc ctctgcgcc gcgccgcgcc cccggcgccc 120
cctccccagc gcgcccccg ccgctcctcc gcgccgcgct cgtcggcc atg gcc cgg 177
                                     Met Ala Arg
                                     1

gag aac ggc gag agc agc tcc tcc tgg aaa aag caa gct gaa gac atc 225
Glu Asn Gly Glu Ser Ser Ser Trp Lys Lys Gln Ala Glu Asp Ile
   5                                10                                15

aag aag atc ttc gag ttc aaa gag acc ctc gga acc ggg gcc ttt tcc 273
Lys Lys Ile Phe Glu Phe Lys Glu Thr Leu Gly Thr Gly Ala Phe Ser
  20                                25                                30                                35

gaa gtg gtt tta gct gaa gag aag gca act ggc aag ctc ttt gct gtg 321
Glu Val Val Leu Ala Glu Glu Lys Ala Thr Gly Lys Leu Phe Ala Val
                                40                                45                                50

aag tgt atc cct aag aag gcg ctg aag ggc aag gaa agc agc ata gag 369
Lys Cys Ile Pro Lys Lys Ala Leu Lys Gly Lys Glu Ser Ser Ile Glu
                                55                                60                                65

aat gag ata gcc gtc ctg aga aag att aag cat gaa aat att gtt gcc 417
Asn Glu Ile Ala Val Leu Arg Lys Ile Lys His Glu Asn Ile Val Ala
                                70                                75                                80

ctg gaa gac att tat gaa agc cca aat cac ctg tac ttg gtc atg cag 465
Leu Glu Asp Ile Tyr Glu Ser Pro Asn His Leu Tyr Leu Val Met Gln
                                85                                90                                95

ctg gtg tcc ggt gga gag ctg ttt gac cgg ata gtg gag aag ggg ttt 513
Leu Val Ser Gly Gly Glu Leu Phe Asp Arg Ile Val Glu Lys Gly Phe
100                                105                                110                                115

tat aca gag aag gat gcc agc act ctg atc cgc caa gtc ttg gac gcc 561
Tyr Thr Glu Lys Asp Ala Ser Thr Leu Ile Arg Gln Val Leu Asp Ala
                                120                                125                                130

gtg tac tat ctc cac aga atg ggc atc gtc cac aga gac ctc aag ccc 609
Val Tyr Tyr Leu His Arg Met Gly Ile Val His Arg Asp Leu Lys Pro
                                135                                140                                145

gaa aat ctc ttg tac tac agt caa gat gag gag tcc aaa ata atg atc 657
Glu Asn Leu Leu Tyr Tyr Ser Gln Asp Glu Glu Ser Lys Ile Met Ile
                                150                                155                                160

agt gac ttt gga ttg tca aaa atg gag ggc aaa gga gat gtg atg tcc 705
Ser Asp Phe Gly Leu Ser Lys Met Glu Gly Lys Gly Asp Val Met Ser
165                                170                                175

```

act gcc tgt gga act cca ggc tat gtc gct cct gaa gtc ctc gcc cag 753
 Thr Ala Cys Gly Thr Pro Gly Tyr Val Ala Pro Glu Val Leu Ala Gln
 180 185 190 195

aaa cct tac agc aaa gcc gtt gac tgc tgg tcc atc gga gtg att gcc 801
 Lys Pro Tyr Ser Lys Ala Val Asp Cys Trp Ser Ile Gly Val Ile Ala
 200 205 210

tac atc ttg ctc tgc ggc tac cct cct ttt tat gat gaa aat gac tcc 849
 Tyr Ile Leu Leu Cys Gly Tyr Pro Pro Phe Tyr Asp Glu Asn Asp Ser
 215 220 225

aag ctc ttt gag cag atc ctc aag gcg gaa tat gag ttt gac tct ccc 897
 Lys Leu Phe Glu Gln Ile Leu Lys Ala Glu Tyr Glu Phe Asp Ser Pro
 230 235 240

tac tgg gat gac atc tcc gac tct gca aaa gac ttc att cgg aac ctg 945
 Tyr Trp Asp Asp Ile Ser Asp Ser Ala Lys Asp Phe Ile Arg Asn Leu
 245 250 255

atg gag aag gac ccg aat aaa aga tac acg tgt gag cag gca gct cgg 993
 Met Glu Lys Asp Pro Asn Lys Arg Tyr Thr Cys Glu Gln Ala Ala Arg
 260 265 270 275

cac cca tgg atc gct ggt gac aca gcc ctc aac aaa aac atc cac gag 1041
 His Pro Trp Ile Ala Gly Asp Thr Ala Leu Asn Lys Asn Ile His Glu
 280 285 290

tcc gtc agc gcc cag atc cgg aaa aac ttt gcc aag agc aaa tgg aga 1089
 Ser Val Ser Ala Gln Ile Arg Lys Asn Phe Ala Lys Ser Lys Trp Arg
 295 300 305

caa gca ttt aat gcc acg gcc gtc gtg aga cat atg aga aaa cta cac 1137
 Gln Ala Phe Asn Ala Thr Ala Val Val Arg His Met Arg Lys Leu His
 310 315 320

ctc ggc agc agc ctg gac agt tca aat gca agt gtt tcg agc agc ctc 1185
 Leu Gly Ser Ser Leu Asp Ser Ser Asn Ala Ser Val Ser Ser Ser Leu
 325 330 335

agt ttg gcc agc caa aaa gac tgt gcg tat gta gca aaa cca gaa tcc 1233
 Ser Leu Ala Ser Gln Lys Asp Cys Ala Tyr Val Ala Lys Pro Glu Ser
 340 345 350 355

ctc agc tga cactgaagac gagcctggggg tggagaggag ggagccggca 1282
 Leu Ser *

tctgccgagc acctcctgtt tgccaggcgc tttctatact taatcccatg tcatgcgacc 1342
 ctaggacttt ttttaacatg taatcactgg gccgggtgca gtggctcacg cctgtaatcc 1402
 caacactttg ggaggctgag gcaggaggac tgtttgagtt caggagtttt aagaccagcc 1462
 tgaccaacat ggtgaaaccc catctctact aaaatataaa aattagccgg gtgtggtggc 1522
 gagcacctgt aatgtcagct acttgggagg ctgaggcagg agaatcactt gaaccagga 1582
 agcggagggt gcaatgagct gagatcacac cactgcactc cagcctgggt gacagattga 1642
 gactccctct caaaaaaaaaa agggaaatca ttgaacactc gtggaaccct aggtattgca 1702
 tattccattt acggtttggg aatccagggc tcaagtctc gcagggggtac cgagctcgag 1762
 atcgtaatca 1772

<210> 33
 <211> 357

<212> PRT

<213> Homo sapiens

<400> 33

```
Met Ala Arg Glu Asn Gly Glu Ser Ser Ser Ser Trp Lys Lys Gln Ala
 1          5          10          15
Glu Asp Ile Lys Lys Ile Phe Glu Phe Lys Glu Thr Leu Gly Thr Gly
 20          25          30
Ala Phe Ser Glu Val Val Leu Ala Glu Glu Lys Ala Thr Gly Lys Leu
 35          40          45
Phe Ala Val Lys Cys Ile Pro Lys Lys Ala Leu Lys Gly Lys Glu Ser
 50          55          60
Ser Ile Glu Asn Glu Ile Ala Val Leu Arg Lys Ile Lys His Glu Asn
 65          70          75          80
Ile Val Ala Leu Glu Asp Ile Tyr Glu Ser Pro Asn His Leu Tyr Leu
 85          90          95
Val Met Gln Leu Val Ser Gly Gly Glu Leu Phe Asp Arg Ile Val Glu
100          105          110
Lys Gly Phe Tyr Thr Glu Lys Asp Ala Ser Thr Leu Ile Arg Gln Val
115          120          125
Leu Asp Ala Val Tyr Tyr Leu His Arg Met Gly Ile Val His Arg Asp
130          135          140
Leu Lys Pro Glu Asn Leu Leu Tyr Tyr Ser Gln Asp Glu Glu Ser Lys
145          150          155          160
Ile Met Ile Ser Asp Phe Gly Leu Ser Lys Met Glu Gly Lys Gly Asp
165          170          175
Val Met Ser Thr Ala Cys Gly Thr Pro Gly Tyr Val Ala Pro Glu Val
180          185          190
Leu Ala Gln Lys Pro Tyr Ser Lys Ala Val Asp Cys Trp Ser Ile Gly
195          200          205
Val Ile Ala Tyr Ile Leu Leu Cys Gly Tyr Pro Pro Phe Tyr Asp Glu
210          215          220
Asn Asp Ser Lys Leu Phe Glu Gln Ile Leu Lys Ala Glu Tyr Glu Phe
225          230          235          240
Asp Ser Pro Tyr Trp Asp Asp Ile Ser Asp Ser Ala Lys Asp Phe Ile
245          250          255
Arg Asn Leu Met Glu Lys Asp Pro Asn Lys Arg Tyr Thr Cys Glu Gln
260          265          270
Ala Ala Arg His Pro Trp Ile Ala Gly Asp Thr Ala Leu Asn Lys Asn
275          280          285
Ile His Glu Ser Val Ser Ala Gln Ile Arg Lys Asn Phe Ala Lys Ser
290          295          300
Lys Trp Arg Gln Ala Phe Asn Ala Thr Ala Val Val Arg His Met Arg
305          310          315          320
Lys Leu His Leu Gly Ser Ser Leu Asp Ser Ser Asn Ala Ser Val Ser
325          330          335
Ser Ser Leu Ser Leu Ala Ser Gln Lys Asp Cys Ala Tyr Val Ala Lys
340          345          350
Pro Glu Ser Leu Ser
355
```

<210> 34

<211> 1074

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1074)

<400> 34

atg gcc cgg gag aac ggc gag agc agc tcc tcc tgg aaa aag caa gct	48
Met Ala Arg Glu Asn Gly Glu Ser Ser Ser Ser Trp Lys Lys Gln Ala	
1 5 10 15	
gaa gac atc aag aag atc ttc gag ttc aaa gag acc ctc gga acc ggg	96
Glu Asp Ile Lys Lys Ile Phe Glu Phe Lys Glu Thr Leu Gly Thr Gly	
20 25 30	
gcc ttt tcc gaa gtg gtt tta gct gaa gag aag gca act ggc aag ctc	144
Ala Phe Ser Glu Val Val Leu Ala Glu Glu Lys Ala Thr Gly Lys Leu	
35 40 45	
ttt gct gtg aag tgt atc cct aag aag gcg ctg aag ggc aag gaa agc	192
Phe Ala Val Lys Cys Ile Pro Lys Lys Ala Leu Lys Gly Lys Glu Ser	
50 55 60	
agc ata gag aat gag ata gcc gtc ctg aga aag att aag cat gaa aat	240
Ser Ile Glu Asn Glu Ile Ala Val Leu Arg Lys Ile Lys His Glu Asn	
65 70 75 80	
att gtt gcc ctg gaa gac att tat gaa agc cca aat cac ctg tac ttg	288
Ile Val Ala Leu Glu Asp Ile Tyr Glu Ser Pro Asn His Leu Tyr Leu	
85 90 95	
gtc atg cag ctg gtg tcc ggt gga gag ctg ttt gac cgg ata gtg gag	336
Val Met Gln Leu Val Ser Gly Gly Glu Leu Phe Asp Arg Ile Val Glu	
100 105 110	
aag ggg ttt tat aca gag aag gat gcc agc act ctg atc cgc caa gtc	384
Lys Gly Phe Tyr Thr Glu Lys Asp Ala Ser Thr Leu Ile Arg Gln Val	
115 120 125	
ttg gac gcc gtg tac tat ctc cac aga atg ggc atc gtc cac aga gac	432
Leu Asp Ala Val Tyr Tyr Leu His Arg Met Gly Ile Val His Arg Asp	
130 135 140	
ctc aag ccc gaa aat ctc ttg tac tac agt caa gat gag gag tcc aaa	480
Leu Lys Pro Glu Asn Leu Leu Tyr Tyr Ser Gln Asp Glu Glu Ser Lys	
145 150 155 160	
ata atg atc agt gac ttt gga ttg tca aaa atg gag ggc aaa gga gat	528
Ile Met Ile Ser Asp Phe Gly Leu Ser Lys Met Glu Gly Lys Gly Asp	
165 170 175	
gtg atg tcc act gcc tgt gga act cca ggc tat gtc gct cct gaa gtc	576
Val Met Ser Thr Ala Cys Gly Thr Pro Gly Tyr Val Ala Pro Glu Val	
180 185 190	
ctc gcc cag aaa cct tac agc aaa gcc gtt gac tgc tgg tcc atc gga	624
Leu Ala Gln Lys Pro Tyr Ser Lys Ala Val Asp Cys Trp Ser Ile Gly	
195 200 205	
gtg att gcc tac atc ttg ctc tgc ggc tac cct cct ttt tat gat gaa	672
Val Ile Ala Tyr Ile Leu Leu Cys Gly Tyr Pro Pro Phe Tyr Asp Glu	
210 215 220	
aat gac tcc aag ctc ttt gag cag atc ctc aag gcg gaa tat gag ttt	720
Asn Asp Ser Lys Leu Phe Glu Gln Ile Leu Lys Ala Glu Tyr Glu Phe	
225 230 235 240	

gac tct ccc tac tgg gat gac atc tcc gac tct gca aaa gac ttc att	768
Asp Ser Pro Tyr Trp Asp Asp Ile Ser Asp Ser Ala Lys Asp Phe Ile	
245 250 255	
cgg aac ctg atg gag aag gac ccg aat aaa aga tac acg tgt gag cag	816
Arg Asn Leu Met Glu Lys Asp Pro Asn Lys Arg Tyr Thr Cys Glu Gln	
260 265 270	
gca gct cgg cac cca tgg atc gct ggt gac aca gcc ctc aac aaa aac	864
Ala Ala Arg His Pro Trp Ile Ala Gly Asp Thr Ala Leu Asn Lys Asn	
275 280 285	
atc cac gag tcc gtc agc gcc cag atc cgg aaa aac ttt gcc aag agc	912
Ile His Glu Ser Val Ser Ala Gln Ile Arg Lys Asn Phe Ala Lys Ser	
290 295 300	
aaa tgg aga caa gca ttt aat gcc acg gcc gtc gtg aga cat atg aga	960
Lys Trp Arg Gln Ala Phe Asn Ala Thr Ala Val Val Arg His Met Arg	
305 310 315 320	
aaa cta cac ctc ggc agc agc ctg gac agt tca aat gca agt gtt tcg	1008
Lys Leu His Leu Gly Ser Ser Leu Asp Ser Ser Asn Ala Ser Val Ser	
325 330 335	
agc agc ctc agt ttg gcc agc caa aaa gac tgt gcg tat gta gca aaa	1056
Ser Ser Leu Ser Leu Ala Ser Gln Lys Asp Cys Ala Tyr Val Ala Lys	
340 345 350	
cca gaa tcc ctc agc tga	1074
Pro Glu Ser Leu Ser *	
355	

<210> 35
 <211> 3579
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1213) ... (3159)

<400> 35	
aacagttctg tcacttggtc gacatttaat acatgtgagt tgtatgaatg cctaaaggcc	60
ataccatgct gcctgggaaa cagcaagaac tccatcagtg gcagagacta tcactattat	120
tacattaaaa acaaccctga tatcaagcca gttgaaaatg gaccttgag ggaaaaagta	180
cgagaaacca tgaaggatca agttcagcga aatgaggaca aatctactac cttgaaattg	240
gctgattttg gacttgcaaa gcatgtggtg agacctatat ttactgtgtg tgggacccca	300
acttacgtag ctcccgaat tctttctgag aaagggttatg gactggaggt ggacatgtgg	360
gctgctggcg tgatcctcta tatcctgctg tgtggctttc cccattccg cagccctgag	420
agggaccagg acgagctctt taacatcatc cagctgggcc actttgagtt cctccccct	480
tactgggaca atatctctga tgctgctaaa gatctggtga gccggttgct ggtggtagac	540
cccaaaaagc gctacacagc tcatcaggtt cttcagcacc cctggatcga aacagctggc	600
aagaccaata cagtgaacg acagaagcag gtgtcccccgc gcagcgaggg tcacttccgg	660
agccagcaca agagggttgt ggagcaggta tcatatcygc tgagggtctca agatgtgtct	720
cttaaagccc caaattccca ctcaacttct catagccatt atgactgatt tagctgaata	780
accttgggac agcaaggcct atgtgacctt tctctaaaat atttaagctc gagaatcaca	840
gagcggaagc tgcaaggctc ctggctgcct gccagccgag ggaatctgga gaaaccattc	900
ctggggccgc gtggcccccgt cgtgcccttg ttctgccctc ggaatggcct tcactcagca	960
catcctgaga acagccctct gaagcccagg gtcgtgaccg tagtgaagct ggggtgggcag	1020
cgcccccgaa agatcactct gctcctcaac aggcgatcag tgcagacgtt cgagcagctc	1080

ttagctgaca	tctcagaagc	cttgggctct	cccgatgga	agaatgaccg	tgtgaggaaa	1140
ctgtttaacc	tcaagggcag	ggaaatcagg	agcgtctctg	atttcttcag	ggaaggggat	1200
gctttcatag	ct atg ggc	aaa gaa cca	ctg aca ctg	aag agc att	cag gtg	1251
	Met Gly Lys	Glu Pro Leu	Thr Leu Lys	Ser Ile Gln	Val	
	1		5		10	
gct gta gaa gaa ctg tac	ccc aac aaa gcc	cgg gcc ctg aca	ctg gcc		1299	
Ala Val Glu Glu Leu Tyr	Pro Asn Lys Ala Arg	Ala Leu Thr Leu Ala				
	15	20	25			
cag cac agc cgt gcc cct	tct cca agg ctg agg	agc agg ctg ttt	agc		1347	
Gln His Ser Arg Ala Pro	Ser Pro Arg Leu Arg	Ser Arg Leu Phe	Ser			
	30	35	40	45		
aag gct ctg aaa gga gac	cac cgc tgt ggg gag	acc gag acc ccc	aag		1395	
Lys Ala Leu Lys Gly Asp	His Arg Cys Gly Glu Thr	Glu Thr Pro Lys				
	50	55	60			
agc tgc agc gaa gtt gca	gga tgc aag gca gcc	atg agg cac cag	ggg		1443	
Ser Cys Ser Glu Val Ala	Gly Cys Lys Ala Ala	Met Arg His Gln	Gly			
	65	70	75			
aag atc ccc gag gag ctt	tca cta gat gac aga	gcg agg acc cag	aag		1491	
Lys Ile Pro Glu Glu Leu	Ser Leu Asp Asp Arg	Ala Thr Gln Lys				
	80	85	90			
aag tgg ggg agg ggg aaa	tgg gag cca gaa ccc	agt agc aag ccc	ccc		1539	
Lys Trp Gly Arg Gly Lys	Trp Glu Pro Glu Pro	Ser Ser Lys Pro Pro				
	95	100	105			
agg gaa gcc act ctg gaa	gag agg cac gca agg	gga gag aag cat	ctt		1587	
Arg Glu Ala Thr Leu Glu	Glu Arg His Ala Arg	Gly Glu Lys His	Leu			
	110	115	120	125		
ggg gtg gag att gaa aag	acc tcg ggt gaa att	atc aga tgc gag	aag		1635	
Gly Val Glu Ile Glu Lys	Thr Ser Gly Glu Ile	Ile Arg Cys Glu	Lys			
	130	135	140			
tgc aag aga gag agg gag	ctc cag cag agc ctg	gag cgt gag agg	ctt		1683	
Cys Lys Arg Glu Arg Glu	Leu Gln Gln Ser Leu	Glu Arg Glu Arg	Leu			
	145	150	155			
tct ctg ggg acc agt gag	ctg gat atg ggg aag	ggc cca atg tat	gat		1731	
Ser Leu Gly Thr Ser Glu	Leu Asp Met Gly Lys	Gly Pro Met Tyr	Asp			
	160	165	170			
gtg gag aag ctg gtg agg	acc aga agc tgc agg	agg tct ccc gag	gca		1779	
Val Glu Lys Leu Val Arg	Thr Arg Ser Cys Arg	Arg Ser Pro Glu	Ala			
	175	180	185			
aat cct gca agt ggg gag	gaa ggg tgg aag ggt	gac agc cac agg	agc		1827	
Asn Pro Ala Ser Gly Glu	Glu Gly Trp Lys Gly	Asp Ser His Arg	Ser			
	190	195	200	205		
agc ccc agg aat ccc act	caa gag ctg agg aga	ccc agc aag agc	atg		1875	
Ser Pro Arg Asn Pro Thr	Gln Glu Leu Arg Arg	Pro Ser Lys Ser	Met			
	210	215	220			
gac aag aaa gag gac aga	ggc cca gag gat	caa gaa agc cat	gct		1923	
Asp Lys Lys Glu Asp Arg	Gly Pro Glu Asp	Gln Glu Ser His	Gln			
	225	230	235			

gga gca gcc aag gcc aag aag gac ctt gtg gaa gtt ctt cct gtc aca	1971
Gly Ala Ala Lys Ala Lys Lys Asp Leu Val Glu Val Leu Pro Val Thr	
240 245 250	
gag gag ggg ctg agg gag gtg aag aag gac acc agg ccc atg agc agg	2019
Glu Glu Gly Leu Arg Glu Val Lys Lys Asp Thr Arg Pro Met Ser Arg	
255 260 265	
agc aaa cat ggt ggc tgg ctc ctg aga gag cac cag gcg ggc ttt gag	2067
Ser Lys His Gly Gly Trp Leu Leu Arg Glu His Gln Ala Gly Phe Glu	
270 275 280 285	
aag ctc cgc agg acc cga gga gaa gag aag gag gca gag aag gag aaa	2115
Lys Leu Arg Arg Thr Arg Gly Glu Glu Lys Glu Ala Glu Lys Glu Lys	
290 295 300	
aag cca tgt atg tct gga ggc aga agg atg act ctc aga gat gac caa	2163
Lys Pro Cys Met Ser Gly Gly Arg Arg Met Thr Leu Arg Asp Asp Gln	
305 310 315	
cct gca aag cta gaa aag gag ccc aag acg agg cca gaa gag aac aag	2211
Pro Ala Lys Leu Glu Lys Glu Pro Lys Thr Arg Pro Glu Glu Asn Lys	
320 325 330	
cca gag cgg ccc agc ggt cgg aag cca cgg ccc atg ggc atc att gcc	2259
Pro Glu Arg Pro Ser Gly Arg Lys Pro Arg Pro Met Gly Ile Ile Ala	
335 340 345	
gcc aat gtg gaa aag cat tat gag act ggc cgg gtc att ggg gat ggg	2307
Ala Asn Val Glu Lys His Tyr Glu Thr Gly Arg Val Ile Gly Asp Gly	
350 355 360 365	
aac ttt gct gtc gtg aag gag tgc aga cac cgc gag acc agg cag gcc	2355
Asn Phe Ala Val Val Lys Glu Cys Arg His Arg Glu Thr Arg Gln Ala	
370 375 380	
tat gcg atg aag atc att gac aag tcc aga ctc aag ggc aag gag gac	2403
Tyr Ala Met Lys Ile Ile Asp Lys Ser Arg Leu Lys Gly Lys Glu Asp	
385 390 395	
atg gtg gac agt gag atc ttg atc atc cag agc ctc tct cac ccc aac	2451
Met Val Asp Ser Glu Ile Leu Ile Ile Gln Ser Leu Ser His Pro Asn	
400 405 410	
atc gtg aaa ttg cat gaa gtc tac gaa aca gac atg gaa atc tac ctg	2499
Ile Val Lys Leu His Glu Val Tyr Glu Thr Asp Met Glu Ile Tyr Leu	
415 420 425	
atc ctg gag tac gtg cag gga gga gac ctt ttt gac gcc atc ata gaa	2547
Ile Leu Glu Tyr Val Gln Gly Gly Asp Leu Phe Asp Ala Ile Ile Glu	
430 435 440 445	
agt gtg aag ttc ccg gag ccc gat gct gcc ctc atg atc atg gac tta	2595
Ser Val Lys Phe Pro Glu Pro Asp Ala Ala Leu Met Ile Met Asp Leu	
450 455 460	
tgc aaa gcc ctc gtc cac atg cac gac aag agc att gtc cac cgg gac	2643
Cys Lys Ala Leu Val His Met His Asp Lys Ser Ile Val His Arg Asp	
465 470 475	

ctc aag ccg gaa aac ctt ttg gtt cag cga aat gag gac aaa tct act	2691
Leu Lys Pro Glu Asn Leu Leu Val Gln Arg Asn Glu Asp Lys Ser Thr	
480 485 490	
acc ttg aaa ttg gct gat ttt gga ctt gca aag cat gtg gtg aga cct	2739
Thr Leu Lys Leu Ala Asp Phe Gly Leu Ala Lys His Val Val Arg Pro	
495 500 505	
ata ttt act gtg tgt ggg acc cca act tac gta gct ccc gaa att ctt	2787
Ile Phe Thr Val Cys Gly Thr Pro Thr Tyr Val Ala Pro Glu Ile Leu	
510 515 520 525	
tct gag aaa ggt tat gga ctg gag gtg gac atg tgg gct gct ggc gtg	2835
Ser Glu Lys Gly Tyr Gly Leu Glu Val Asp Met Trp Ala Ala Gly Val	
530 535 540	
atc ctc tat atc ctg ctg tgt ggc ttt ccc cca ttc cgc agc cct gag	2883
Ile Leu Tyr Ile Leu Leu Cys Gly Phe Pro Pro Phe Arg Ser Pro Glu	
545 550 555	
agg gac cag gac gag ctc ttt aac atc atc cag ctg ggc cac ttt gag	2931
Arg Asp Gln Asp Glu Leu Phe Asn Ile Ile Gln Leu Gly His Phe Glu	
560 565 570	
ttc ctc ccc cct tac tgg gac aat atc tct gat gct gct aaa gat ctg	2979
Phe Leu Pro Pro Tyr Trp Asp Asn Ile Ser Asp Ala Ala Lys Asp Leu	
575 580 585	
gtg agc cgg ttg ctg gtg gta gac ccc aaa aag cgc tac aca gct cat	3027
Val Ser Arg Leu Leu Val Val Asp Pro Lys Lys Arg Tyr Thr Ala His	
590 595 600 605	
cag gtt ctt cag cac ccc tgg atc gaa aca gct ggc aag acc aat aca	3075
Gln Val Leu Gln His Pro Trp Ile Glu Thr Ala Gly Lys Thr Asn Thr	
610 615 620	
gtg aaa cga cag aag cag gtg tcc ccc agc agc gag ggt cac ttc cgg	3123
Val Lys Arg Gln Lys Gln Val Ser Pro Ser Ser Glu Gly His Phe Arg	
625 630 635	
agc cag cac aag agg gtt gtg gag cag gta tca tag tcaccacctt	3169
Ser Gln His Lys Arg Val Val Glu Gln Val Ser *	
640 645	
gggaatctgt ccagccccc gttctgtctca aggacagaga aaaggataga agtttgagag	3229
aaaaacaatg aaagaggctt cttcacataa ttggtgaatc agaggggagag aactgagta	3289
tattttaaag catattaaaa aaattaagtc aatgttaaat gtcacaacat atttttagat	3349
ttgtatatatt aaagccttta atacattttt ggggggtaag cattgtcatc agtgaggaat	3409
tttggttaata atgatgtgtt ttgcttcccc tttgtwacca agttttattct gtactacagg	3469
agtgggtgctt accaggggtct aaactcccc tgtgagatta ataaggtgca ttgtggtctt	3529
tctgtgttaa taaaatgtgc tctgaataac agaagcgtaa attaaaaaaaa	3579

<210> 36

<211> 648

<212> PRT

<213> Homo sapiens

<400> 36

Met Gly Lys Glu Pro Leu Thr Leu Lys Ser Ile Gln Val Ala Val Glu
1 5 10 15
Glu Leu Tyr Pro Asn Lys Ala Arg Ala Leu Thr Leu Ala Gln His Ser

Val	Cys	Gly	Thr	Pro	Thr	Tyr	Val	Ala	Pro	Glu	Ile	Leu	Ser	Glu	Lys
		515					520					525			
Gly	Tyr	Gly	Leu	Glu	Val	Asp	Met	Trp	Ala	Ala	Gly	Val	Ile	Leu	Tyr
	530					535					540				
Ile	Leu	Leu	Cys	Gly	Phe	Pro	Pro	Phe	Arg	Ser	Pro	Glu	Arg	Asp	Gln
545					550					555					560
Asp	Glu	Leu	Phe	Asn	Ile	Ile	Gln	Leu	Gly	His	Phe	Glu	Phe	Leu	Pro
				565					570					575	
Pro	Tyr	Trp	Asp	Asn	Ile	Ser	Asp	Ala	Ala	Lys	Asp	Leu	Val	Ser	Arg
			580					585					590		
Leu	Leu	Val	Val	Asp	Pro	Lys	Lys	Arg	Tyr	Thr	Ala	His	Gln	Val	Leu
		595					600					605			
Gln	His	Pro	Trp	Ile	Glu	Thr	Ala	Gly	Lys	Thr	Asn	Thr	Val	Lys	Arg
	610					615					620				
Gln	Lys	Gln	Val	Ser	Pro	Ser	Ser	Glu	Gly	His	Phe	Arg	Ser	Gln	His
625					630					635					640
Lys	Arg	Val	Val	Glu	Gln	Val	Ser								
				645											

<210> 37
 <211> 1947
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1947)

<400> 37																
atg	ggc	aaa	gaa	cca	ctg	aca	ctg	aag	agc	att	cag	gtg	gct	gta	gaa	48
Met	Gly	Lys	Glu	Pro	Leu	Thr	Leu	Lys	Ser	Ile	Gln	Val	Ala	Val	Glu	
1				5					10					15		
gaa ctg tac ccc aac aaa gcc cgg gcc ctg aca ctg gcc cag cac agc															96	
Glu	Leu	Tyr	Pro	Asn	Lys	Ala	Arg	Ala	Leu	Thr	Leu	Ala	Gln	His	Ser	
			20					25					30			
cgt gcc cct tct cca agg ctg agg agc agg ctg ttt agc aag gct ctg															144	
Arg	Ala	Pro	Ser	Pro	Arg	Leu	Arg	Ser	Arg	Leu	Phe	Ser	Lys	Ala	Leu	
			35				40					45				
aaa gga gac cac cgc tgt ggg gag acc gag acc ccc aag agc tgc agc															192	
Lys	Gly	Asp	His	Arg	Cys	Gly	Glu	Thr	Glu	Thr	Pro	Lys	Ser	Cys	Ser	
	50					55					60					
gaa gtt gca gga tgc aag gca gcc atg agg cac cag ggg aag atc ccc															240	
Glu	Val	Ala	Gly	Cys	Lys	Ala	Ala	Met	Arg	His	Gln	Gly	Lys	Ile	Pro	
	65				70					75					80	
gag gag ctt tca cta gat gac aga gcg agg acc cag aag aag tgg ggg															288	
Glu	Glu	Leu	Ser	Leu	Asp	Asp	Arg	Ala	Arg	Thr	Gln	Lys	Lys	Trp	Gly	
				85					90					95		
agg ggg aaa tgg gag cca gaa ccc agt agc aag ccc ccc agg gaa gcc															336	
Arg	Gly	Lys	Trp	Glu	Pro	Glu	Pro	Ser	Ser	Lys	Pro	Pro	Arg	Glu	Ala	
			100					105					110			
act ctg gaa gag agg cac gca agg gga gag aag cat ctt ggg gtg gag															384	
Thr	Leu	Glu	Glu	Arg	His	Ala	Arg	Gly	Glu	Lys	His	Leu	Gly	Val	Glu	
		115					120					125				

att gaa aag acc tcg ggt gaa att atc aga tgc gag aag tgc aag aga Ile Glu Lys Thr Ser Gly Glu Ile Ile Arg Cys Glu Lys Cys Lys Arg 130 135 140	432
gag agg gag ctc cag cag agc ctg gag cgt gag agg ctt tct ctg ggg Glu Arg Glu Leu Gln Gln Ser Leu Glu Arg Glu Arg Leu Ser Leu Gly 145 150 155 160	480
acc agt gag ctg gat atg ggg aag ggc cca atg tat gat gtg gag aag Thr Ser Glu Leu Asp Met Gly Lys Gly Pro Met Tyr Asp Val Glu Lys 165 170 175	528
ctg gtg agg acc aga agc tgc agg agg tct ccc gag gca aat cct gca Leu Val Arg Thr Arg Ser Cys Arg Arg Ser Pro Glu Ala Asn Pro Ala 180 185 190	576
agt ggg gag gaa ggg tgg aag ggt gac agc cac agg agc agc ccc agg Ser Gly Glu Glu Gly Trp Lys Gly Asp Ser His Arg Ser Ser Pro Arg 195 200 205	624
aat ccc act caa gag ctg agg aga ccc agc aag agc atg gac aag aaa Asn Pro Thr Gln Glu Leu Arg Arg Pro Ser Lys Ser Met Asp Lys Lys 210 215 220	672
gag gac aga ggc cca gag gat caa gaa agc cat gct cag gga gca gcc Glu Asp Arg Gly Pro Glu Asp Gln Glu Ser His Ala Gln Gly Ala Ala 225 230 235 240	720
aag gcc aag aag gac ctt gtg gaa gtt ctt cct gtc aca gag gag ggg Lys Ala Lys Lys Asp Leu Val Glu Val Leu Pro Val Thr Glu Glu Gly 245 250 255	768
ctg agg gag gtg aag aag gac acc agg ccc atg agc agg agc aaa cat Leu Arg Glu Val Lys Lys Asp Thr Arg Pro Met Ser Arg Ser Lys His 260 265 270	816
ggt ggc tgg ctc ctg aga gag cac cag gcg ggc ttt gag aag ctc cgc Gly Gly Trp Leu Leu Arg Glu His Gln Ala Gly Phe Glu Lys Leu Arg 275 280 285	864
agg acc cga gga gaa gag aag gag gca gag aag gag aaa aag cca tgt Arg Thr Arg Gly Glu Glu Lys Glu Ala Glu Lys Glu Lys Lys Pro Cys 290 295 300	912
atg tct gga ggc aga agg atg act ctc aga gat gac caa cct gca aag Met Ser Gly Gly Arg Arg Met Thr Leu Arg Asp Asp Gln Pro Ala Lys 305 310 315 320	960
cta gaa aag gag ccc aag acg agg cca gaa gag aac aag cca gag cgg Leu Glu Lys Glu Pro Lys Thr Arg Pro Glu Glu Asn Lys Pro Glu Arg 325 330 335	1008
ccc agc ggt cgg aag cca cgg ccc atg ggc atc att gcc gcc aat gtg Pro Ser Gly Arg Lys Pro Arg Pro Met Gly Ile Ile Ala Ala Asn Val 340 345 350	1056
gaa aag cat tat gag act ggc cgg gtc att ggg gat ggg aac ttt gct Glu Lys His Tyr Glu Thr Gly Arg Val Ile Gly Asp Gly Asn Phe Ala 355 360 365	1104

gtc	gtg	aag	gag	tgc	aga	cac	cgc	gag	acc	agg	cag	gcc	tat	gcg	atg	1152
Val	Val	Lys	Glu	Cys	Arg	His	Arg	Glu	Thr	Arg	Gln	Ala	Tyr	Ala	Met	
	370					375					380					
aag	atc	att	gac	aag	tcc	aga	ctc	aag	ggc	aag	gag	gac	atg	gtg	gac	1200
Lys	Ile	Ile	Asp	Lys	Ser	Arg	Leu	Lys	Gly	Lys	Glu	Asp	Met	Val	Asp	
385					390					395					400	
agt	gag	atc	ttg	atc	atc	cag	agc	ctc	tct	cac	ccc	aac	atc	gtg	aaa	1248
Ser	Glu	Ile	Leu	Ile	Ile	Gln	Ser	Leu	Ser	His	Pro	Asn	Ile	Val	Lys	
				405					410					415		
ttg	cat	gaa	gtc	tac	gaa	aca	gac	atg	gaa	atc	tac	ctg	atc	ctg	gag	1296
Leu	His	Glu	Val	Tyr	Glu	Thr	Asp	Met	Glu	Ile	Tyr	Leu	Ile	Leu	Glu	
			420					425						430		
tac	gtg	cag	gga	gga	gac	ctt	ttt	gac	gcc	atc	ata	gaa	agt	gtg	aag	1344
Tyr	Val	Gln	Gly	Gly	Asp	Leu	Phe	Asp	Ala	Ile	Ile	Glu	Ser	Val	Lys	
		435				440						445				
ttc	ccg	gag	ccc	gat	gct	gcc	ctc	atg	atc	atg	gac	tta	tgc	aaa	gcc	1392
Phe	Pro	Glu	Pro	Asp	Ala	Ala	Leu	Met	Ile	Met	Asp	Leu	Cys	Lys	Ala	
	450					455					460					
ctc	gtc	cac	atg	cac	gac	aag	agc	att	gtc	cac	cgg	gac	ctc	aag	ccg	1440
Leu	Val	His	Met	His	Asp	Lys	Ser	Ile	Val	His	Arg	Asp	Leu	Lys	Pro	
465					470					475					480	
gaa	aac	ctt	ttg	gtt	cag	cga	aat	gag	gac	aaa	tct	act	acc	ttg	aaa	1488
Glu	Asn	Leu	Leu	Val	Gln	Arg	Asn	Glu	Asp	Lys	Ser	Thr	Thr	Leu	Lys	
				485					490					495		
ttg	gct	gat	ttt	gga	ctt	gca	aag	cat	gtg	gtg	aga	cct	ata	ttt	act	1536
Leu	Ala	Asp	Phe	Gly	Leu	Ala	Lys	His	Val	Val	Arg	Pro	Ile	Phe	Thr	
			500					505					510			
gtg	tgt	ggg	acc	cca	act	tac	gta	gct	ccc	gaa	att	ctt	tct	gag	aaa	1584
Val	Cys	Gly	Thr	Pro	Thr	Tyr	Val	Ala	Pro	Glu	Ile	Leu	Ser	Glu	Lys	
		515					520					525				
ggc	tat	gga	ctg	gag	gtg	gac	atg	tgg	gct	gct	ggc	gtg	atc	ctc	tat	1632
Gly	Tyr	Gly	Leu	Glu	Val	Asp	Met	Trp	Ala	Ala	Gly	Val	Ile	Leu	Tyr	
	530					535					540					
atc	ctg	ctg	tgt	ggc	ttt	ccc	cca	ttc	cgc	agc	cct	gag	agg	gac	cag	1680
Ile	Leu	Leu	Cys	Gly	Phe	Pro	Pro	Phe	Arg	Ser	Pro	Glu	Arg	Asp	Gln	
545					550					555					560	
gac	gag	ctc	ttt	aac	atc	atc	cag	ctg	ggc	cac	ttt	gag	ttc	ctc	ccc	1728
Asp	Glu	Leu	Phe	Asn	Ile	Ile	Gln	Leu	Gly	His	Phe	Glu	Phe	Leu	Pro	
				565					570					575		
cct	tac	tgg	gac	aat	atc	tct	gat	gct	gct	aaa	gat	ctg	gtg	agc	cgg	1776
Pro	Tyr	Trp	Asp	Asn	Ile	Ser	Asp	Ala	Ala	Lys	Asp	Leu	Val	Ser	Arg	
			580					585					590			
ttg	ctg	gtg	gta	gac	ccc	aaa	aag	cgc	tac	aca	gct	cat	cag	gtt	ctt	1824
Leu	Leu	Val	Val	Asp	Pro	Lys	Lys	Arg	Tyr	Thr	Ala	His	Gln	Val	Leu	
		595					600					605				
cag	cac	ccc	tgg	atc	gaa	aca	gct	ggc	aag	acc	aat	aca	gtg	aaa	cga	1872

Gln	His	Pro	Trp	Ile	Glu	Thr	Ala	Gly	Lys	Thr	Asn	Thr	Val	Lys	Arg		
610						615					620						
cag	aag	cag	gtg	tcc	ccc	agc	agc	gag	ggg	cac	ttc	cgg	agc	cag	cac	1920	
Gln	Lys	Gln	Val	Ser	Pro	Ser	Ser	Glu	Gly	His	Phe	Arg	Ser	Gln	His		
625					630					635					640		
aag	agg	gtt	gtg	gag	cag	gta	tca	tag								1947	
Lys	Arg	Val	Val	Glu	Gln	Val	Ser	*									
				645													

<210> 38
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Consensus sequence involved in ATP binding
 (Prosite Accession No. PS00107)

<221> VARIANT
 <222> (1)...(1)
 <223> Leu can be Ile or Val.

<221> VARIANT
 <222> (3)...(3)
 <223> Xaa can be any amino acid except Pro.

<221> VARIANT
 <222> (5)...(5)
 <223> Xaa can be any amino acid except Pro.

<221> VARIANT
 <222> (6)...(6)
 <223> Phe can be Tyr, Trp, Met, Gly, Ser, Thr, Asn, or His.

<221> VARIANT
 <222> (7)...(7)
 <223> Ser can be Gly or Ala.

<221> VARIANT
 <222> (8)...(8)
 <223> Xaa can be any amino acid except Pro or Trp.

<221> VARIANT
 <222> (9)...(9)
 <223> Leu can be Ile, Val, Cys, Ala, or Thr.

<221> VARIANT
 <222> (10)...(10)
 <223> Xaa can be any amino acid except Pro or Asp.

<221> VARIANT
 <222> (11)...(11)
 <223> Xaa = Any Amino Acid.

<221> VARIANT
 <222> (12)...(12)
 <223> Gly can be Ser, Thr, Ala, Cys, Leu, Ile, Val, Met, Phe, or Tyr.

<221> VARIANT
 <222> (13)...(13)
 <223> Xaa can be any amino acid and as few as 5 and as many as 18 amino acids.

<221> VARIANT
 <222> (14)...(14)
 <223> Leu can be Ile, Val, Met, Phe, Tyr, Trp, Cys, Ser, Thr, Ala, or Arg.

<221> VARIANT
 <222> (15)...(15)
 <223> Ala can be Ile, Val, or Pro.

<221> VARIANT
 <222> (16)...(16)
 <223> Leu can be Ile, Val, Met, Phe, Ala, Gly, Cys, Lys, or Arg.

<221> BINDING
 <222> (17)...(17)

<400> 38
 Leu Gly Xaa Gly Xaa Phe Ser Xaa Leu Xaa Xaa Gly Xaa Leu Ala Leu
 1 5 10 15
 Lys

<210> 39
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Consensus sequence for serine/threonine kinases
 (Prosite Accession No. PS00108)

<221> VARIANT
 <222> (1)...(1)
 <223> Leu can be Ile, Val, Met, Phe, or Tyr.

<221> VARIANT
 <222> (2)...(2)

<223> Xaa = Any Amino Acid

<221> VARIANT
 <222> (3)...(3)
 <223> His can be Tyr.

<221> VARIANT
 <222> (4)...(4)
 <223> Xaa = Any Amino Acid

<221> ACT_SITE

<222> (5)...(5)
 <221> VARIANT
 <222> (6)...(6)
 <223> Leu can be Ile, Val, Met, Phe, or Tyr.
 <221> VARIANT
 <222> (8)...(9)
 <223> Xaa = Any Amino Acid.
 <221> VARIANT
 <222> (11)...(11)
 <223> Leu can be Ile, Val, Met, Phe, Tyr, Cys, or Thr.
 <221> VARIANT
 <222> (12)...(12)
 <223> Leu can be Ile, Val, Met, Phe, Tyr, Cys, or Thr.
 <221> VARIANT
 <222> (13)...(13)
 <223> Leu can be Ile, Val, Met, Phe, Tyr, Cys, or Thr.
 <400> 39
 Leu Xaa His Xaa Asp Leu Lys Xaa Xaa Asn Leu Leu Leu
 1 5 10
 <210> 40
 <211> 13
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Consensus Sequence for tyrosine kinase (Prosite
 Accession No. PS00109)
 <221> VARIANT
 <222> (1)...(1)
 <223> Leu can be Ile, Val, Met, Phe, Tyr, or Cys.
 <221> VARIANT
 <222> (2)...(2)
 <223> Xaa = Any Amino Acid
 <221> VARIANT
 <222> (3)...(3)
 <223> His can be Tyr.
 <221> VARIANT
 <222> (4)...(4)
 <223> Xaa = Any Amino Acid
 <221> ACT_SITE
 <222> (5)...(5)
 <221> VARIANT
 <222> (6)...(6)
 <223> Leu can be Ile, Val, Met, Phe, or Tyr.
 <221> VARIANT
 <222> (7)...(7)

<223> Arg can be Ser, Thr, Ala, or Cys.
 <221> VARIANT
 <222> (8)...(9)
 <223> Xaa = Any Amino Acid.
 <221> VARIANT
 <222> (11)...(11)
 <223> Leu can be Ile, Val, Met, Phe, Tyr, or Cys.
 <221> VARIANT
 <222> (12)...(12)
 <223> Leu can be Ile, Val, Met, Phe, Tyr, or Cys.
 <221> VARIANT
 <222> (13)...(13)
 <223> Leu can be Ile, Val, Met, Phe, Tyr, or Cys.
 <400> 40
 Leu Xaa His Xaa Asp Leu Arg Xaa Xaa Asn Leu Leu Leu
 1 5 10
 <210> 41
 <211> 5
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Consensus Sequence for tyrosine kinase
 phosphorylation site (Prosite Accession No.
 PS00007)
 <221> VARIANT
 <222> (1)...(1)
 <223> Arg can be Lys.
 <221> VARIANT
 <222> (2)...(2)
 <223> Xaa can be any amino acid and can be two or three
 amino acids.
 <221> VARIANT
 <222> (3)...(3)
 <223> Asp can be Glu.
 <221> VARIANT
 <222> (4)...(4)
 <223> Xaa can be any amino acid and can be two or three
 amino acids.
 <221> PHOSPHORYLATION
 <222> (5)...(5)
 <400> 41
 Arg Xaa Asp Xaa Tyr
 1 5
 <210> 42
 <211> 29

<212> PRT
<213> Artificial Sequence

<220>
<223> ATP-binding region signature sequence

<400> 42
Leu Gly Thr Gly Ala Phe Ser Glu Val Val Leu Ala Glu Glu Lys Ala
1 5 10 15
Thr Gly Lys Leu Phe Ala Val Lys Cys Ile Pro Lys Lys
20 25

<210> 43
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Serine/threonine kinase active-site signature
sequence

<400> 43
Ile Val His Arg Asp Leu Lys Pro Glu Asn Leu Leu Tyr
1 5 10

<210> 44
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Serine/threonine kinase active-site signature
sequence

<400> 44
Ile Val His Arg Asp Leu Lys Pro Glu Asn Leu Leu Val
1 5 10

<210> 45
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Tyrosine kinase phosphorylation site

<400> 45
Arg Ile Val Glu Lys Gly Phe Tyr
1 5

<210> 46
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Tyrosine kinase phosphorylation site

<400> 46
 Arg Gln Val Leu Asp Ala Val Tyr Tyr
 1 5

<210> 47
 <211> 3164
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(2877)

<400> 47
 atg ccg gtc cgc agg ggc cac gtc gct ccc caa aac act tac ctg gac 48
 Met Pro Val Arg Arg Gly His Val Ala Pro Gln Asn Thr Tyr Leu Asp
 1 5 10 15
 acc atc atc cgc aag ttc gag ggc caa agt cgg aag ttc ctg att gcc 96
 Thr Ile Ile Arg Lys Phe Glu Gly Gln Ser Arg Lys Phe Leu Ile Ala
 20 25 30
 aat gct cag atg gag aac tgc gcc atc att tac tgc aac gac ggc ttc 144
 Asn Ala Gln Met Glu Asn Cys Ala Ile Ile Tyr Cys Asn Asp Gly Phe
 35 40 45
 tgc gaa ctc ttc ggc tac tcc cga gtg gag gtg atg cag caa ccc tgc 192
 Cys Glu Leu Phe Gly Tyr Ser Arg Val Glu Val Met Gln Gln Pro Cys
 50 55 60
 acc tgc gac ttc ctc aca ggc ccc aac aca cca agc agc gcc gtg tcc 240
 Thr Cys Asp Phe Leu Thr Gly Pro Asn Thr Pro Ser Ser Ala Val Ser
 65 70 75 80
 cgc cta gcg cag gcc ctg ctg ggg gct gag gag tgc aag gtg gac atc 288
 Arg Leu Ala Gln Ala Leu Leu Gly Ala Glu Glu Cys Lys Val Asp Ile
 85 90 95
 ctc tac tac cgc aag gat gcc tcc agc ttc cgc tgc ctg gta gat gtg 336
 Leu Tyr Tyr Arg Lys Asp Ala Ser Ser Phe Arg Cys Leu Val Asp Val
 100 105 110
 gtg ccc gtg aag aac gag gac ggg gct gtc atc atg ttc att ctc aac 384
 Val Pro Val Lys Asn Glu Asp Gly Ala Val Ile Met Phe Ile Leu Asn
 115 120 125
 ttc gag gac ctg gcc cag ctc ctg gcc aag tgc agc agc cgc agc ttg 432
 Phe Glu Asp Leu Ala Gln Leu Leu Ala Lys Cys Ser Ser Arg Ser Leu
 130 135 140
 tcc cag cgc ctg ttg tcc cag agc ttc ctg ggc tcc gag ggc tct cat 480
 Ser Gln Arg Leu Leu Ser Gln Ser Phe Leu Gly Ser Glu Gly Ser His
 145 150 155 160
 ggc agg cca ggc gga cca ggg cca ggc aca ggc agg ggc aag tac agg 528
 Gly Arg Pro Gly Gly Pro Gly Pro Gly Thr Gly Arg Gly Lys Tyr Arg
 165 170 175
 acc atc agc cag atc cca cag ttc acg ctc aac ttc gtg gag ttc aac 576

Thr	Ile	Ser	Gln	Ile	Pro	Gln	Phe	Thr	Leu	Asn	Phe	Val	Glu	Phe	Asn		
			180					185					190				
ttg	gag	aag	cac	cgc	tcc	agc	tcc	acc	acg	gag	att	gag	atc	atc	gcg	624	
Leu	Glu	Lys	His	Arg	Ser	Ser	Ser	Thr	Thr	Glu	Ile	Glu	Ile	Ile	Ala		
		195					200					205					
ccc	cat	aag	gtg	gtg	gag	cgg	aca	cag	aac	gtc	act	gag	aag	gtc	acc	672	
Pro	His	Lys	Val	Val	Glu	Arg	Thr	Gln	Asn	Val	Thr	Glu	Lys	Val	Thr		
	210					215					220						
cag	gtc	ctg	tcc	ctg	ggc	gcg	gat	gtg	ctg	ccg	gag	tac	aag	ctg	cag	720	
Gln	Val	Leu	Ser	Leu	Gly	Ala	Asp	Val	Leu	Pro	Glu	Tyr	Lys	Leu	Gln		
225					230					235					240		
gcg	ccg	cgc	atc	cac	cgc	tgg	acc	atc	ctg	cac	tac	agc	ccc	ttc	aag	768	
Ala	Pro	Arg	Ile	His	Arg	Trp	Thr	Ile	Leu	His	Tyr	Ser	Pro	Phe	Lys		
				245					250					255			
gcc	gtg	tgg	gac	tgg	ctc	atc	ctg	ctg	ctg	gtc	atc	tac	acg	gct	gtc	816	
Ala	Val	Trp	Asp	Trp	Leu	Ile	Leu	Leu	Leu	Val	Ile	Tyr	Thr	Ala	Val		
			260					265					270				
ttc	acg	ccc	tac	tca	gcc	gcc	ttc	ctg	ctc	agc	gac	cag	gac	gaa	tca	864	
Phe	Thr	Pro	Tyr	Ser	Ala	Ala	Phe	Leu	Leu	Ser	Asp	Gln	Asp	Glu	Ser		
		275					280					285					
cgg	cgt	ggg	gcc	tgc	agc	tat	acc	tgc	agt	ccc	ctc	act	gtg	gtg	gat	912	
Arg	Arg	Gly	Ala	Cys	Ser	Tyr	Thr	Cys	Ser	Pro	Leu	Thr	Val	Val	Asp		
	290					295					300						
ctc	atc	gtg	gac	atc	atg	ttc	gtc	gtg	gac	atc	gtc	atc	aac	ttc	cgc	960	
Leu	Ile	Val	Asp	Ile	Met	Phe	Val	Val	Asp	Ile	Val	Ile	Asn	Phe	Arg		
305					310					315					320		
acc	acc	tat	gtc	aac	acc	aat	gat	gag	gtg	gtc	agc	cac	ccc	cgc	cgc	1008	
Thr	Thr	Tyr	Val	Asn	Thr	Asn	Asp	Glu	Val	Val	Ser	His	Pro	Arg	Arg		
				325				330						335			
atc	gcc	gtc	cac	tac	ttc	aag	ggc	tgg	ttc	ctc	att	gac	atg	gtg	gcc	1056	
Ile	Ala	Val	His	Tyr	Phe	Lys	Gly	Trp	Phe	Leu	Ile	Asp	Met	Val	Ala		
			340					345					350				
gcc	atc	cct	ttc	gac	ctc	ctg	atc	ttc	cgc	act	ggc	tcc	gat	gag	acc	1104	
Ala	Ile	Pro	Phe	Asp	Leu	Leu	Ile	Phe	Arg	Thr	Gly	Ser	Asp	Glu	Thr		
		355					360					365					
aca	acc	ctg	att	ggg	cta	ttg	aag	aca	gcg	cgg	ctg	ctg	cgg	ctg	gtg	1152	
Thr	Thr	Leu	Ile	Gly	Leu	Leu	Lys	Thr	Ala	Arg	Leu	Leu	Arg	Leu	Val		
	370					375					380						
cgc	gta	gca	cgg	aag	ctg	gac	cgc	tac	tct	gag	tat	ggg	gcg	gct	gtg	1200	
Arg	Val	Ala	Arg	Lys	Leu	Asp	Arg	Tyr	Ser	Glu	Tyr	Gly	Ala	Ala	Val		
385					390					395					400		
ctc	ttc	ttg	ctc	atg	tgc	acc	ttc	gcg	ctc	ata	gcg	cac	tgg	ctg	gcc	1248	
Leu	Phe	Leu	Leu	Met	Cys	Thr	Phe	Ala	Leu	Ile	Ala	His	Trp	Leu	Ala		
				405				410						415			
tgc	atc	tgg	tac	gcc	atc	ggc	aat	gtg	gag	cgg	ccc	tac	cta	gaa	cac	1296	
Cys	Ile	Trp	Tyr	Ala	Ile	Gly	Asn	Val	Glu	Arg	Pro	Tyr	Leu	Glu	His		

420	425	430	
aag atc ggc tgg ctg gac agc ctg ggt gtg cag ctt ggc aag cgc tac Lys Ile Gly Trp Leu Asp Ser Leu Gly Val Gln Leu Gly Lys Arg Tyr 435 440 445			1344
aac ggc agc gac cca gcc tcg ggc ccc tcg gtg cag gac aag tat gtc Asn Gly Ser Asp Pro Ala Ser Gly Pro Ser Val Gln Asp Lys Tyr Val 450 455 460			1392
aca gcc ctc tac ttc acc ttc agc agc ctc acc agc gtg ggc ttc ggc Thr Ala Leu Tyr Phe Thr Phe Ser Ser Leu Thr Ser Val Gly Phe Gly 465 470 475 480			1440
aat gtc tcg ccc aac acc aac tcc gag aag gtc ttc tcc atc tgc gtc Asn Val Ser Pro Asn Thr Asn Ser Glu Lys Val Phe Ser Ile Cys Val 485 490 495			1488
atg ctc atc ggc tcc ctg atg tac gcc agc atc ttc ggg aac gtg tcc Met Leu Ile Gly Ser Leu Met Tyr Ala Ser Ile Phe Gly Asn Val Ser 500 505 510			1536
gcg atc atc cag cgc ctg tac tcg ggc acc gcg cgc tac cac acg cag Ala Ile Ile Gln Arg Leu Tyr Ser Gly Thr Ala Arg Tyr His Thr Gln 515 520 525			1584
atg ctg cgt gtc aag gag ttc atc cgc ttc cac cag atc ccc aac cca Met Leu Arg Val Lys Glu Phe Ile Arg Phe His Gln Ile Pro Asn Pro 530 535 540			1632
ctg cgc cag cgc ctg gag gag tat ttc cag cac gcc tgg tcc tac acc Leu Arg Gln Arg Leu Glu Glu Tyr Phe Gln His Ala Trp Ser Tyr Thr 545 550 555 560			1680
aat ggc att gac atg aac gcg gtg ctg aag ggc ttc ccc gag tgc ctg Asn Gly Ile Asp Met Asn Ala Val Leu Lys Gly Phe Pro Glu Cys Leu 565 570 575			1728
cag gct gac atc tgc ctg cac ctg cac cgc gca ctg ctg cag cac tgc Gln Ala Asp Ile Cys Leu His Leu His Arg Ala Leu Leu Gln His Cys 580 585 590			1776
cca gct ttc agc ggc gcc ggc aag ggc tgc ctg cgc gcg cta gcc gtc Pro Ala Phe Ser Gly Ala Gly Lys Gly Cys Leu Arg Ala Leu Ala Val 595 600 605			1824
aag ttc aag acc acc cac gcg ccg cct ggg gac acg ctg gtg cac ctc Lys Phe Lys Thr Thr His Ala Pro Pro Gly Asp Thr Leu Val His Leu 610 615 620			1872
ggc gac gtg ctc tcc acc ctc tac ttc atc tcc cga ggc tcc atc gag Gly Asp Val Leu Ser Thr Leu Tyr Phe Ile Ser Arg Gly Ser Ile Glu 625 630 635 640			1920
atc ctg cgc gac gac gtg gtc gtg gcc atc cta gga aag aat gac atc Ile Leu Arg Asp Asp Val Val Val Ala Ile Leu Gly Lys Asn Asp Ile 645 650 655			1968
ttt ggg gaa ccc gtc agc ctc cat gcc cag cca ggc aag tcc agt gca Phe Gly Glu Pro Val Ser Leu His Ala Gln Pro Gly Lys Ser Ser Ala 660 665 670			2016

gac	gtg	cgg	gct	ctg	acc	tac	tgc	gac	ctg	cac	aag	atc	cag	cgg	gca	2064
Asp	Val	Arg	Ala	Leu	Thr	Tyr	Cys	Asp	Leu	His	Lys	Ile	Gln	Arg	Ala	
		675					680					685				
gat	ctg	ctg	gag	gtg	ctg	gac	atg	tac	ccg	gcc	ttt	gcg	gag	agc	ttc	2112
Asp	Leu	Leu	Glu	Val	Leu	Asp	Met	Tyr	Pro	Ala	Phe	Ala	Glu	Ser	Phe	
	690					695					700					
tgg	agt	aag	ctg	gag	gtc	acc	ttc	aac	ctg	cgg	gac	gca	gcc	ggg	ggc	2160
Trp	Ser	Lys	Leu	Glu	Val	Thr	Phe	Asn	Leu	Arg	Asp	Ala	Ala	Gly	Gly	
705					710					715					720	
ctc	cac	tca	tcc	ccc	cga	cag	gct	cct	ggc	agc	caa	gac	cac	caa	ggc	2208
Leu	His	Ser	Ser	Pro	Arg	Gln	Ala	Pro	Gly	Ser	Gln	Asp	His	Gln	Gly	
				725					730					735		
ttc	ttt	ctc	agt	gac	aac	cag	tca	gat	gca	gcc	cct	ccc	ctg	agc	atc	2256
Phe	Phe	Leu	Ser	Asp	Asn	Gln	Ser	Asp	Ala	Ala	Pro	Pro	Leu	Ser	Ile	
			740					745					750			
tca	gat	gca	tct	ggc	ctc	tgg	cct	gag	cta	ctg	cag	gaa	atg	ccc	cca	2304
Ser	Asp	Ala	Ser	Gly	Leu	Trp	Pro	Glu	Leu	Leu	Gln	Glu	Met	Pro	Pro	
		755					760					765				
agg	cac	agc	ccc	caa	agc	cct	cag	gaa	gac	cca	gat	tgc	tgg	cct	ctg	2352
Arg	His	Ser	Pro	Gln	Ser	Pro	Gln	Glu	Asp	Pro	Asp	Cys	Trp	Pro	Leu	
	770					775					780					
aag	ctg	ggc	tcc	agg	cta	gag	cag	ctc	cag	gcc	cag	atg	aac	agg	ctg	2400
Lys	Leu	Gly	Ser	Arg	Leu	Glu	Gln	Leu	Gln	Ala	Gln	Met	Asn	Arg	Leu	
785					790					795					800	
gag	tcc	cgc	gtg	tcc	tca	gac	ctc	agc	cgc	atc	ttg	cag	ctc	ctc	cag	2448
Glu	Ser	Arg	Val	Ser	Ser	Asp	Leu	Ser	Arg	Ile	Leu	Gln	Leu	Leu	Gln	
				805					810					815		
aag	ccc	atg	ccc	cag	ggc	cac	gcc	agc	tac	att	ctg	gaa	gcc	cct	gcc	2496
Lys	Pro	Met	Pro	Gln	Gly	His	Ala	Ser	Tyr	Ile	Leu	Glu	Ala	Pro	Ala	
			820					825					830			
tcc	aat	gac	ctg	gcc	ttg	gtt	cct	ata	gcc	tcg	gag	acg	acg	agt	cca	2544
Ser	Asn	Asp	Leu	Ala	Leu	Val	Pro	Ile	Ala	Ser	Glu	Thr	Thr	Ser	Pro	
		835					840					845				
ggg	ccc	agg	ctg	ccc	cag	ggc	ttt	ctg	cct	cct	gca	cag	acc	cca	agc	2592
Gly	Pro	Arg	Leu	Pro	Gln	Gly	Phe	Leu	Pro	Pro	Ala	Gln	Thr	Pro	Ser	
	850					855					860					
tat	gga	gac	ttg	gat	gac	tgt	agt	cca	aag	cac	agg	aac	tcc	tcc	ccc	2640
Tyr	Gly	Asp	Leu	Asp	Asp	Cys	Ser	Pro	Lys	His	Arg	Asn	Ser	Ser	Pro	
865					870					875					880	
agg	atg	cct	cac	ctg	gct	gtg	gca	acg	gac	aaa	act	ctg	gca	cca	tcc	2688
Arg	Met	Pro	His	Leu	Ala	Val	Ala	Thr	Asp	Lys	Thr	Leu	Ala	Pro	Ser	
				885					890					895		
tca	gaa	cag	gaa	cag	cct	gag	ggg	ctc	tgg	cca	ccc	cta	gcc	tca	cct	2736
Ser	Glu	Gln	Glu	Gln	Pro	Glu	Gly	Leu	Trp	Pro	Pro	Leu	Ala	Ser	Pro	
			900					905					910			

cta	cat	ccc	ctg	gaa	gta	caa	gga	ctc	atc	tgt	ggg	ccc	tgc	ttc	tcc	2784
Leu	His	Pro	Leu	Glu	Val	Gln	Gly	Leu	Ile	Cys	Gly	Pro	Cys	Phe	Ser	
		915					920					925				

tcc	ctc	cct	gaa	cac	ctt	ggc	tct	gtt	ccc	aag	cag	ctg	gac	ttc	cag	2832
Ser	Leu	Pro	Glu	His	Leu	Gly	Ser	Val	Pro	Lys	Gln	Leu	Asp	Phe	Gln	
		930				935					940					

aga	cat	ggc	tca	gat	cct	gga	ttt	gca	ggg	agt	tgg	ggc	cac	tga		2877
Arg	His	Gly	Ser	Asp	Pro	Gly	Phe	Ala	Gly	Ser	Trp	Gly	His	*		
		945				950				955						

actccaagat	aaagacacca	tgaggggact	gaaggtgggc	aaggggattt	ccttttagctg	2937
ggcatggttg	cgggcgcctg	taatcccagc	tactcaggag	gctgaagcaa	gagaatcact	2997
tgaaccctaa	aggcagaggt	tgcaagtgagc	cgagatagtg	ccactgcact	acagcccggg	3057
cgacagagtg	agactccatc	tcaaaaaataa	aataaaaaaaaa	aaaaaaaaaaaa	aaaaaaaaaaaa	3117
aaaaaaaaaaaa	aaaaaaaaaaaa	aaaaaaaaaaaa	aaaaaaaaaaaa	aaaaaaa		3164

<210> 48
 <211> 958
 <212> PRT
 <213> Homo sapiens

<400> 48															
Met	Pro	Val	Arg	Arg	Gly	His	Val	Ala	Pro	Gln	Asn	Thr	Tyr	Leu	Asp
1				5					10					15	
Thr	Ile	Ile	Arg	Lys	Phe	Glu	Gly	Gln	Ser	Arg	Lys	Phe	Leu	Ile	Ala
			20					25					30		
Asn	Ala	Gln	Met	Glu	Asn	Cys	Ala	Ile	Ile	Tyr	Cys	Asn	Asp	Gly	Phe
		35					40					45			
Cys	Glu	Leu	Phe	Gly	Tyr	Ser	Arg	Val	Glu	Val	Met	Gln	Gln	Pro	Cys
		50				55					60				
Thr	Cys	Asp	Phe	Leu	Thr	Gly	Pro	Asn	Thr	Pro	Ser	Ser	Ala	Val	Ser
					70					75					80
Arg	Leu	Ala	Gln	Ala	Leu	Leu	Gly	Ala	Glu	Glu	Cys	Lys	Val	Asp	Ile
				85				90						95	
Leu	Tyr	Tyr	Arg	Lys	Asp	Ala	Ser	Ser	Phe	Arg	Cys	Leu	Val	Asp	Val
			100					105					110		
Val	Pro	Val	Lys	Asn	Glu	Asp	Gly	Ala	Val	Ile	Met	Phe	Ile	Leu	Asn
			115				120					125			
Phe	Glu	Asp	Leu	Ala	Gln	Leu	Leu	Ala	Lys	Cys	Ser	Ser	Arg	Ser	Leu
		130				135					140				
Ser	Gln	Arg	Leu	Leu	Ser	Gln	Ser	Phe	Leu	Gly	Ser	Glu	Gly	Ser	His
					150					155					160
Gly	Arg	Pro	Gly	Gly	Pro	Gly	Pro	Gly	Thr	Gly	Arg	Gly	Lys	Tyr	Arg
				165					170					175	
Thr	Ile	Ser	Gln	Ile	Pro	Gln	Phe	Thr	Leu	Asn	Phe	Val	Glu	Phe	Asn
			180					185					190		
Leu	Glu	Lys	His	Arg	Ser	Ser	Ser	Thr	Thr	Glu	Ile	Glu	Ile	Ile	Ala
		195						200				205			
Pro	His	Lys	Val	Val	Glu	Arg	Thr	Gln	Asn	Val	Thr	Glu	Lys	Val	Thr
						215					220				
Gln	Val	Leu	Ser	Leu	Gly	Ala	Asp	Val	Leu	Pro	Glu	Tyr	Lys	Leu	Gln
					230					235					240
Ala	Pro	Arg	Ile	His	Arg	Trp	Thr	Ile	Leu	His	Tyr	Ser	Pro	Phe	Lys
				245					250					255	
Ala	Val	Trp	Asp	Trp	Leu	Ile	Leu	Leu	Leu	Val	Ile	Tyr	Thr	Ala	Val
			260					265					270		
Phe	Thr	Pro	Tyr	Ser	Ala	Ala	Phe	Leu	Leu	Ser	Asp	Gln	Asp	Glu	Ser
		275					280					285			
Arg	Arg	Gly	Ala	Cys	Ser	Tyr	Thr	Cys	Ser	Pro	Leu	Thr	Val	Val	Asp

290	295	300
Leu Ile Val Asp Ile Met Phe Val Val Asp Ile Val Ile Asn Phe Arg		
305	310	315
Thr Thr Tyr Val Asn Thr Asn Asp Glu Val Val Ser His Pro Arg Arg		
	325	330
Ile Ala Val His Tyr Phe Lys Gly Trp Phe Leu Ile Asp Met Val Ala		
	340	345
Ala Ile Pro Phe Asp Leu Leu Ile Phe Arg Thr Gly Ser Asp Glu Thr		
	355	360
Thr Thr Leu Ile Gly Leu Leu Lys Thr Ala Arg Leu Leu Arg Leu Val		
	370	375
Arg Val Ala Arg Lys Leu Asp Arg Tyr Ser Glu Tyr Gly Ala Ala Val		
385	390	395
Leu Phe Leu Leu Met Cys Thr Phe Ala Leu Ile Ala His Trp Leu Ala		
	405	410
Cys Ile Trp Tyr Ala Ile Gly Asn Val Glu Arg Pro Tyr Leu Glu His		
	420	425
Lys Ile Gly Trp Leu Asp Ser Leu Gly Val Gln Leu Gly Lys Arg Tyr		
	435	440
Asn Gly Ser Asp Pro Ala Ser Gly Pro Ser Val Gln Asp Lys Tyr Val		
	450	455
Thr Ala Leu Tyr Phe Thr Phe Ser Ser Leu Thr Ser Val Gly Phe Gly		
465	470	475
Asn Val Ser Pro Asn Thr Asn Ser Glu Lys Val Phe Ser Ile Cys Val		
	485	490
Met Leu Ile Gly Ser Leu Met Tyr Ala Ser Ile Phe Gly Asn Val Ser		
	500	505
Ala Ile Ile Gln Arg Leu Tyr Ser Gly Thr Ala Arg Tyr His Thr Gln		
	515	520
Met Leu Arg Val Lys Glu Phe Ile Arg Phe His Gln Ile Pro Asn Pro		
	530	535
Leu Arg Gln Arg Leu Glu Glu Tyr Phe Gln His Ala Trp Ser Tyr Thr		
545	550	555
Asn Gly Ile Asp Met Asn Ala Val Leu Lys Gly Phe Pro Glu Cys Leu		
	565	570
Gln Ala Asp Ile Cys Leu His Leu His Arg Ala Leu Leu Gln His Cys		
	580	585
Pro Ala Phe Ser Gly Ala Gly Lys Gly Cys Leu Arg Ala Leu Ala Val		
	595	600
Lys Phe Lys Thr Thr His Ala Pro Pro Gly Asp Thr Leu Val His Leu		
	610	615
Gly Asp Val Leu Ser Thr Leu Tyr Phe Ile Ser Arg Gly Ser Ile Glu		
625	630	635
Ile Leu Arg Asp Asp Val Val Val Ala Ile Leu Gly Lys Asn Asp Ile		
	645	650
Phe Gly Glu Pro Val Ser Leu His Ala Gln Pro Gly Lys Ser Ser Ala		
	660	665
Asp Val Arg Ala Leu Thr Tyr Cys Asp Leu His Lys Ile Gln Arg Ala		
	675	680
Asp Leu Leu Glu Val Leu Asp Met Tyr Pro Ala Phe Ala Glu Ser Phe		
	690	695
Trp Ser Lys Leu Glu Val Thr Phe Asn Leu Arg Asp Ala Ala Gly Gly		
705	710	715
Leu His Ser Ser Pro Arg Gln Ala Pro Gly Ser Gln Asp His Gln Gly		
	725	730
Phe Phe Leu Ser Asp Asn Gln Ser Asp Ala Ala Pro Pro Leu Ser Ile		
	740	745
Ser Asp Ala Ser Gly Leu Trp Pro Glu Leu Leu Gln Glu Met Pro Pro		
	755	760
Arg His Ser Pro Gln Ser Pro Gln Glu Asp Pro Asp Cys Trp Pro Leu		
	770	775
		780

Lys Leu Gly Ser Arg Leu Glu Gln Leu Gln Ala Gln Met Asn Arg Leu
 785 790 795 800
 Glu Ser Arg Val Ser Ser Asp Leu Ser Arg Ile Leu Gln Leu Leu Gln
 805 810 815
 Lys Pro Met Pro Gln Gly His Ala Ser Tyr Ile Leu Glu Ala Pro Ala
 820 825 830
 Ser Asn Asp Leu Ala Leu Val Pro Ile Ala Ser Glu Thr Thr Ser Pro
 835 840 845
 Gly Pro Arg Leu Pro Gln Gly Phe Leu Pro Pro Ala Gln Thr Pro Ser
 850 855 860
 Tyr Gly Asp Leu Asp Asp Cys Ser Pro Lys His Arg Asn Ser Ser Pro
 865 870 875 880
 Arg Met Pro His Leu Ala Val Ala Thr Asp Lys Thr Leu Ala Pro Ser
 885 890 895
 Ser Glu Gln Glu Gln Pro Glu Gly Leu Trp Pro Pro Leu Ala Ser Pro
 900 905 910
 Leu His Pro Leu Glu Val Gln Gly Leu Ile Cys Gly Pro Cys Phe Ser
 915 920 925
 Ser Leu Pro Glu His Leu Gly Ser Val Pro Lys Gln Leu Asp Phe Gln
 930 935 940
 Arg His Gly Ser Asp Pro Gly Phe Ala Gly Ser Trp Gly His
 945 950 955

<210> 49
 <211> 2877
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(2877)

<400> 49
 atg ccg gtc cgc agg ggc cac gtc gct ccc caa aac act tac ctg gac 48
 Met Pro Val Arg Arg Gly His Val Ala Pro Gln Asn Thr Tyr Leu Asp
 1 5 10 15
 acc atc atc cgc aag ttc gag ggc caa agt cgg aag ttc ctg att gcc 96
 Thr Ile Ile Arg Lys Phe Glu Gly Gln Ser Arg Lys Phe Leu Ile Ala
 20 25 30
 aat gct cag atg gag aac tgc gcc atc att tac tgc aac gac ggc ttc 144
 Asn Ala Gln Met Glu Asn Cys Ala Ile Ile Tyr Cys Asn Asp Gly Phe
 35 40 45
 tgc gaa ctc ttc ggc tac tcc cga gtg gag gtg atg cag caa ccc tgc 192
 Cys Glu Leu Phe Gly Tyr Ser Arg Val Glu Val Met Gln Gln Pro Cys
 50 55 60
 acc tgc gac ttc ctc aca ggc ccc aac aca cca agc agc gcc gtg tcc 240
 Thr Cys Asp Phe Leu Thr Gly Pro Asn Thr Pro Ser Ser Ala Val Ser
 65 70 75 80
 cgc cta gcg cag gcc ctg ctg ggg gct gag gag tgc aag gtg gac atc 288
 Arg Leu Ala Gln Ala Leu Leu Gly Ala Glu Glu Cys Lys Val Asp Ile
 85 90 95
 ctc tac tac cgc aag gat gcc tcc agc ttc cgc tgc ctg gta gat gtg 336
 Leu Tyr Tyr Arg Lys Asp Ala Ser Ser Phe Arg Cys Leu Val Asp Val
 100 105 110

gtg ccc gtg aag aac gag gac ggg gct gtc atc atg ttc att ctc aac	384
Val Pro Val Lys Asn Glu Asp Gly Ala Val Ile Met Phe Ile Leu Asn	
115 120 125	
ttc gag gac ctg gcc cag ctc ctg gcc aag tgc agc agc cgc agc ttg	432
Phe Glu Asp Leu Ala Gln Leu Leu Ala Lys Cys Ser Ser Arg Ser Leu	
130 135 140	
tcc cag cgc ctg ttg tcc cag agc ttc ctg ggc tcc gag ggc tct cat	480
Ser Gln Arg Leu Leu Ser Gln Ser Phe Leu Gly Ser Glu Gly Ser His	
145 150 155 160	
ggc agg cca ggc gga cca ggg cca ggc aca ggc agg ggc aag tac agg	528
Gly Arg Pro Gly Gly Pro Gly Pro Gly Thr Gly Arg Gly Lys Tyr Arg	
165 170 175	
acc atc agc cag atc cca cag ttc acg ctc aac ttc gtg gag ttc aac	576
Thr Ile Ser Gln Ile Pro Gln Phe Thr Leu Asn Phe Val Glu Phe Asn	
180 185 190	
ttg gag aag cac cgc tcc agc tcc acc acg gag att gag atc atc gcg	624
Leu Glu Lys His Arg Ser Ser Ser Thr Thr Glu Ile Glu Ile Ile Ala	
195 200 205	
ccc cat aag gtg gtg gag cgg aca cag aac gtc act gag aag gtc acc	672
Pro His Lys Val Val Glu Arg Thr Gln Asn Val Thr Glu Lys Val Thr	
210 215 220	
cag gtc ctg tcc ctg ggc gcg gat gtg ctg ccg gag tac aag ctg cag	720
Gln Val Leu Ser Leu Gly Ala Asp Val Leu Pro Glu Tyr Lys Leu Gln	
225 230 235 240	
gcg ccg cgc atc cac cgc tgg acc atc ctg cac tac agc ccc ttc aag	768
Ala Pro Arg Ile His Arg Trp Thr Ile Leu His Tyr Ser Pro Phe Lys	
245 250 255	
gcc gtg tgg gac tgg ctc atc ctg ctg ctg gtc atc tac acg gct gtc	816
Ala Val Trp Asp Trp Leu Ile Leu Leu Leu Val Ile Tyr Thr Ala Val	
260 265 270	
ttc acg ccc tac tca gcc gcc ttc ctg ctc agc gac cag gac gaa tca	864
Phe Thr Pro Tyr Ser Ala Ala Phe Leu Leu Ser Asp Gln Asp Glu Ser	
275 280 285	
cgg cgt ggg gcc tgc agc tat acc tgc agt ccc ctc act gtg gtg gat	912
Arg Arg Gly Ala Cys Ser Tyr Thr Cys Ser Pro Leu Thr Val Val Asp	
290 295 300	
ctc atc gtg gac atc atg ttc gtc gtg gac atc gtc atc aac ttc cgc	960
Leu Ile Val Asp Ile Met Phe Val Val Asp Ile Val Ile Asn Phe Arg	
305 310 315 320	
acc acc tat gtc aac acc aat gat gag gtg gtc agc cac ccc cgc cgc	1008
Thr Thr Tyr Val Asn Thr Asn Asp Glu Val Val Ser His Pro Arg Arg	
325 330 335	
atc gcc gtc cac tac ttc aag ggc tgg ttc ctc att gac atg gtg gcc	1056
Ile Ala Val His Tyr Phe Lys Gly Trp Phe Leu Ile Asp Met Val Ala	
340 345 350	

gcc atc cct ttc gac ctc ctg atc ttc cgc act ggc tcc gat gag acc	1104
Ala Ile Pro Phe Asp Leu Leu Ile Phe Arg Thr Gly Ser Asp Glu Thr	
355 360 365	
aca acc ctg att ggg cta ttg aag aca gcg cgg ctg ctg cgg ctg gtg	1152
Thr Thr Leu Ile Gly Leu Leu Lys Thr Ala Arg Leu Leu Arg Leu Val	
370 375 380	
cgc gta gca cgg aag ctg gac cgc tac tct gag tat ggg gcg gct gtg	1200
Arg Val Ala Arg Lys Leu Asp Arg Tyr Ser Glu Tyr Gly Ala Ala Val	
385 390 395 400	
ctc ttc ttg ctc atg tgc acc ttc gcg ctc ata gcg cac tgg ctg gcc	1248
Leu Phe Leu Leu Met Cys Thr Phe Ala Leu Ile Ala His Trp Leu Ala	
405 410 415	
tgc atc tgg tac gcc atc ggc aat gtg gag cgg ccc tac cta gaa cac	1296
Cys Ile Trp Tyr Ala Ile Gly Asn Val Glu Arg Pro Tyr Leu Glu His	
420 425 430	
aag atc ggc tgg ctg gac agc ctg ggt gtg cag ctt ggc aag cgc tac	1344
Lys Ile Gly Trp Leu Asp Ser Leu Gly Val Gln Leu Gly Lys Arg Tyr	
435 440 445	
aac ggc agc gac cca gcc tcg ggc ccc tcg gtg cag gac aag tat gtc	1392
Asn Gly Ser Asp Pro Ala Ser Gly Pro Ser Val Gln Asp Lys Tyr Val	
450 455 460	
aca gcc ctc tac ttc acc ttc agc agc ctc acc agc gtg ggc ttc ggc	1440
Thr Ala Leu Tyr Phe Thr Phe Ser Ser Leu Thr Ser Val Gly Phe Gly	
465 470 475 480	
aat gtc tcg ccc aac acc aac tcc gag aag gtc ttc tcc atc tgc gtc	1488
Asn Val Ser Pro Asn Thr Asn Ser Glu Lys Val Phe Ser Ile Cys Val	
485 490 495	
atg ctc atc ggc tcc ctg atg tac gcc agc atc ttc ggg aac gtg tcc	1536
Met Leu Ile Gly Ser Leu Met Tyr Ala Ser Ile Phe Gly Asn Val Ser	
500 505 510	
gcg atc atc cag cgc ctg tac tcg ggc acc gcg cgc tac cac acg cag	1584
Ala Ile Ile Gln Arg Leu Tyr Ser Gly Thr Ala Arg Tyr His Thr Gln	
515 520 525	
atg ctg cgt gtc aag gag ttc atc cgc ttc cac cag atc ccc aac cca	1632
Met Leu Arg Val Lys Glu Phe Ile Arg Phe His Gln Ile Pro Asn Pro	
530 535 540	
ctg cgc cag cgc ctg gag gag tat ttc cag cac gcc tgg tcc tac acc	1680
Leu Arg Gln Arg Leu Glu Glu Tyr Phe Gln His Ala Trp Ser Tyr Thr	
545 550 555 560	
aat ggc att gac atg aac gcg gtg ctg aag ggc ttc ccc gag tgc ctg	1728
Asn Gly Ile Asp Met Asn Ala Val Leu Lys Gly Phe Pro Glu Cys Leu	
565 570 575	
cag gct gac atc tgc ctg cac ctg cac cgc gca ctg ctg cag cac tgc	1776
Gln Ala Asp Ile Cys Leu His Leu His Arg Ala Leu Leu Gln His Cys	
580 585 590	
cca gct ttc agc ggc gcc ggc aag ggc tgc ctg cgc gcg cta gcc gtc	1824

Pro	Ala	Phe	Ser	Gly	Ala	Gly	Lys	Gly	Cys	Leu	Arg	Ala	Leu	Ala	Val		
		595					600					605					
aag	ttc	aag	acc	acc	cac	gcg	ccg	cct	ggg	gac	acg	ctg	gtg	cac	ctc	1872	
Lys	Phe	Lys	Thr	Thr	His	Ala	Pro	Pro	Gly	Asp	Thr	Leu	Val	His	Leu		
	610					615					620						
ggc	gac	gtg	ctc	tcc	acc	ctc	tac	ttc	atc	tcc	cga	ggc	tcc	atc	gag	1920	
Gly	Asp	Val	Leu	Ser	Thr	Leu	Tyr	Phe	Ile	Ser	Arg	Gly	Ser	Ile	Glu		
	625				630					635					640		
atc	ctg	cgc	gac	gac	gtg	gtc	gtg	gcc	atc	cta	gga	aag	aat	gac	atc	1968	
Ile	Leu	Arg	Asp	Asp	Val	Val	Val	Ala	Ile	Leu	Gly	Lys	Asn	Asp	Ile		
				645					650					655			
ttt	ggg	gaa	ccc	gtc	agc	ctc	cat	gcc	cag	cca	ggc	aag	tcc	agt	gca	2016	
Phe	Gly	Glu	Pro	Val	Ser	Leu	His	Ala	Gln	Pro	Gly	Lys	Ser	Ser	Ala		
			660					665					670				
gac	gtg	cgg	gct	ctg	acc	tac	tgc	gac	ctg	cac	aag	atc	cag	cgg	gca	2064	
Asp	Val	Arg	Ala	Leu	Thr	Tyr	Cys	Asp	Leu	His	Lys	Ile	Gln	Arg	Ala		
		675					680					685					
gat	ctg	ctg	gag	gtg	ctg	gac	atg	tac	ccg	gcc	ttt	gcg	gag	agc	ttc	2112	
Asp	Leu	Leu	Glu	Val	Leu	Asp	Met	Tyr	Pro	Ala	Phe	Ala	Glu	Ser	Phe		
	690					695					700						
tgg	agt	aag	ctg	gag	gtc	acc	ttc	aac	ctg	cgg	gac	gca	gcc	ggg	ggt	2160	
Trp	Ser	Lys	Leu	Glu	Val	Thr	Phe	Asn	Leu	Arg	Asp	Ala	Ala	Gly	Gly		
	705				710				715					720			
ctc	cac	tca	tcc	ccc	cga	cag	gct	cct	ggc	agc	caa	gac	cac	caa	ggt	2208	
Leu	His	Ser	Ser	Pro	Arg	Gln	Ala	Pro	Gly	Ser	Gln	Asp	His	Gln	Gly		
				725					730					735			
ttc	ttt	ctc	agt	gac	aac	cag	tca	gat	gca	gcc	cct	ccc	ctg	agc	atc	2256	
Phe	Phe	Leu	Ser	Asp	Asn	Gln	Ser	Asp	Ala	Ala	Pro	Pro	Leu	Ser	Ile		
			740					745					750				
tca	gat	gca	tct	ggc	ctc	tgg	cct	gag	cta	ctg	cag	gaa	atg	ccc	cca	2304	
Ser	Asp	Ala	Ser	Gly	Leu	Trp	Pro	Glu	Leu	Leu	Gln	Glu	Met	Pro	Pro		
		755					760					765					
agg	cac	agc	ccc	caa	agc	cct	cag	gaa	gac	cca	gat	tgc	tgg	cct	ctg	2352	
Arg	His	Ser	Pro	Gln	Ser	Pro	Gln	Glu	Asp	Pro	Asp	Cys	Trp	Pro	Leu		
	770					775					780						
aag	ctg	ggc	tcc	agg	cta	gag	cag	ctc	cag	gcc	cag	atg	aac	agg	ctg	2400	
Lys	Leu	Gly	Ser	Arg	Leu	Glu	Gln	Leu	Gln	Ala	Gln	Met	Asn	Arg	Leu		
	785				790					795					800		
gag	tcc	cgc	gtg	tcc	tca	gac	ctc	agc	cgc	atc	ttg	cag	ctc	ctc	cag	2448	
Glu	Ser	Arg	Val	Ser	Ser	Asp	Leu	Ser	Arg	Ile	Leu	Gln	Leu	Leu	Gln		
				805					810					815			
aag	ccc	atg	ccc	cag	ggc	cac	gcc	agc	tac	att	ctg	gaa	gcc	cct	gcc	2496	
Lys	Pro	Met	Pro	Gln	Gly	His	Ala	Ser	Tyr	Ile	Leu	Glu	Ala	Pro	Ala		
			820					825					830				
tcc	aat	gac	ctg	gcc	ttg	gtt	cct	ata	gcc	tcg	gag	acg	acg	agt	cca	2544	
Ser	Asn	Asp	Leu	Ala	Leu	Val	Pro	Ile	Ala	Ser	Glu	Thr	Thr	Ser	Pro		

835	840	845	
ggg ccc agg ctg ccc cag ggc ttt ctg cct cct gca cag acc cca agc			2592
Gly Pro Arg Leu Pro Gln Gly Phe Leu Pro Pro Ala Gln Thr Pro Ser			
850	855	860	
tat gga gac ttg gat gac tgt agt cca aag cac agg aac tcc tcc ccc			2640
Tyr Gly Asp Leu Asp Asp Cys Ser Pro Lys His Arg Asn Ser Ser Pro			
865	870	875	880
agg atg cct cac ctg gct gtg gca acg gac aaa act ctg gca cca tcc			2688
Arg Met Pro His Leu Ala Val Ala Thr Asp Lys Thr Leu Ala Pro Ser			
	885	890	895
tca gaa cag gaa cag cct gag ggg ctc tgg cca ccc cta gcc tca cct			2736
Ser Glu Gln Glu Gln Pro Glu Gly Leu Trp Pro Pro Leu Ala Ser Pro			
	900	905	910
cta cat ccc ctg gaa gta caa gga ctc atc tgt ggt ccc tgc ttc tcc			2784
Leu His Pro Leu Glu Val Gln Gly Leu Ile Cys Gly Pro Cys Phe Ser			
	915	920	925
tcc ctc cct gaa cac ctt ggc tct gtt ccc aag cag ctg gac ttc cag			2832
Ser Leu Pro Glu His Leu Gly Ser Val Pro Lys Gln Leu Asp Phe Gln			
	930	935	940
aga cat ggc tca gat cct gga ttt gca ggg agt tgg ggc cac tga			2877
Arg His Gly Ser Asp Pro Gly Phe Ala Gly Ser Trp Gly His *			
945	950	955	

<210> 50
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PAS domain

<400> 50
 Ile Leu Tyr Trp Asn Ala Ala Ala Glu Glu Leu Thr Gly Leu Ser Arg
 1 5 10 15
 Glu Glu Val

<210> 51
 <211> 43
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PAC domain

<400> 51
 Thr Leu Glu Tyr Arg Asn Leu Arg Lys Asp Gly Ser Leu Ile Trp Val
 1 5 10 15
 Leu Val Ser Ala Ser Pro Ile Arg Asp Glu Asp Gly Glu Val Leu Gly
 20 25 30
 Ile Val Gly Val Ile Arg Asp Ile Thr Glu Arg

<210> 52
 <211> 254
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Cyclic nucleotide gated channel transmembrane
 region domain

<400> 52

Tyr	Leu	Lys	Ser	Thr	Trp	Phe	Leu	Leu	Asp	Val	Leu	Ser	Thr	Leu	Pro
1				5					10					15	
Phe	Asp	Leu	Leu	Tyr	Ile	Phe	Phe	Gly	Ser	Asp	Glu	Gly	Ser	Gly	Gly
		20						25					30		
Ser	Leu	Phe	Pro	Leu	Leu	Arg	Leu	Asn	Arg	Leu	Leu	Arg	Leu	Arg	Arg
		35					40					45			
Val	Phe	Glu	Leu	Phe	Asp	Arg	Leu	Glu	Thr	Asp	Thr	Ala	Phe	Asn	Tyr
	50					55					60				
Phe	Ala	Phe	Arg	Leu	Ala	Lys	Leu	Val	Cys	Val	Ile	Leu	Leu	Ile	Ile
65					70					75					80
His	Trp	Asn	Ala	Cys	Ile	Tyr	Tyr	Ala	Ile	Ser	Asp	Tyr	Asp	Val	Glu
			85						90					95	
Ala	Glu	Val	Tyr	Gly	Phe	Gly	Thr	Asp	Thr	Trp	Leu	Tyr	Ala	Leu	Asn
		100						105					110		
Pro	Asp	Phe	Glu	Glu	Pro	Ser	Leu	Trp	Ile	Arg	Gly	Ile	Ile	Gly	Gly
		115					120					125			
Pro	Ser	Leu	Lys	Arg	Gln	Tyr	Ile	Thr	Ser	Leu	Tyr	Trp	Ser	Ile	Thr
	130					135					140				
Thr	Leu	Thr	Thr	Val	Gly	Tyr	Gly	Asp	Pro	Ala	Pro	Val	Thr	Thr	Arg
145					150					155					160
Glu	Lys	Ile	Phe	Val	Ile	Phe	Asp	Met	Leu	Phe	Gly	Val	Leu	Leu	Phe
			165					170						175	
Ala	Tyr	Ile	Ile	Gly	Asn	Val	Thr	Ser	Ile	Val	Val	Asn	Met	Asn	Ser
		180						185					190		
Arg	Thr	Ala	Glu	Phe	Arg	Thr	Lys	Met	Asp	Ala	Val	Lys	Glu	Phe	Met
	195						200					205			
Lys	Phe	Arg	Lys	Leu	Pro	Lys	Arg	Leu	Gln	Glu	Arg	Val	Leu	Lys	Tyr
	210					215					220				
Phe	Glu	Tyr	Thr	Trp	Ser	Asn	Lys	Ser	Asp	Glu	Gly	Leu	Asp	Glu	Glu
225					230					235					240
Glu	Val	Leu	Glu	Gln	Leu	Pro	Lys	Lys	Leu	Arg	Ala	Glu	Ile		
			245						250						

<210> 53
 <211> 114
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Cyclic nucleotide binding domain (CNBD)

<400> 53

Ala	Leu	Glu	Glu	Arg	Arg	Tyr	Pro	Ala	Pro	Gly	Glu	Tyr	Ile	Ile	Arg
1				5					10					15	
Gln	Gly	Asp	Pro	Gly	Asp	Ser	Phe	Tyr	Ile	Ile	Val	Ser	Gly	Arg	Val
		20						25					30		
Glu	Val	Tyr	Lys	Glu	Thr	Glu	Asp	Gly	Ser	Thr	Pro	Gly	Glu	Ser	Gly

Ile	Ala	Val	His	Tyr	Phe	Lys	Gly	Trp	Phe	Leu	Ile	Asp	Met	Val	Ala
			340					345					350		
Ala	Ile	Pro	Phe	Asp	Leu	Leu	Ile	Phe	Arg	Thr	Gly	Ser	Asp	Glu	Thr
		355					360					365			
Thr	Thr	Leu	Ile	Gly	Leu	Leu	Lys	Thr	Ala	Arg	Leu	Leu	Arg	Leu	Val
	370					375					380				
Arg	Val	Ala	Arg	Lys	Leu	Asp	Arg	Tyr	Ser	Glu	Tyr	Gly	Ala	Ala	Val
385					390					395					400
Leu	Phe	Leu	Leu	Met	Cys	Thr	Phe	Ala	Leu	Ile	Ala	His	Trp	Leu	Ala
				405					410					415	
Cys	Ile	Trp	Tyr	Ala	Ile	Gly	Asn	Val	Glu	Arg	Pro	Tyr	Leu	Glu	His
			420					425					430		
Lys	Ile	Gly	Trp	Leu	Asp	Ser	Leu	Gly	Val	Gln	Leu	Gly	Lys	Arg	Tyr
		435					440					445			
Asn	Gly	Ser	Asp	Pro	Ala	Ser	Gly	Pro	Ser	Val	Gln	Asp	Lys	Tyr	Val
	450					455					460				
Thr	Ala	Leu	Tyr	Phe	Thr	Phe	Ser	Ser	Leu	Thr	Ser	Val	Gly	Phe	Gly
465					470					475					480
Asn	Val	Ser	Pro	Asn	Thr	Asn	Ser	Glu	Lys	Val	Phe	Ser	Ile	Cys	Val
				485					490					495	
Met	Leu	Ile	Gly	Ser	Leu	Met	Tyr	Ala	Ser	Ile	Phe	Gly	Asn	Val	Ser
			500					505					510		
Ala	Ile	Ile	Gln	Arg	Leu	Tyr	Ser	Gly	Thr	Ala	Arg	Tyr	His	Thr	Gln
		515					520					525			
Met	Leu	Arg	Val	Lys	Glu	Phe	Ile	Arg	Phe	His	Gln	Ile	Pro	Asn	Pro
	530					535					540				
Leu	Arg	Gln	Arg	Leu	Glu	Glu	Tyr	Phe	Gln	His	Ala	Trp	Ser	Tyr	Thr
545					550					555					560
Asn	Gly	Ile	Asp	Met	Asn	Ala	Val	Leu	Lys	Gly	Phe	Pro	Glu	Cys	Leu
			565					570						575	
Gln	Ala	Asp	Ile	Cys	Leu	His	Leu	His	Arg	Ala	Leu	Leu	Gln	His	Cys
			580					585					590		
Pro	Ala	Phe	Ser	Gly	Ala	Gly	Lys	Gly	Cys	Leu	Arg	Ala	Leu	Ala	Val
		595					600					605			
Lys	Phe	Lys	Thr	Thr	His	Ala	Pro	Pro	Gly	Asp	Thr	Leu	Val	His	Leu
	610					615					620				
Gly	Asp	Val	Leu	Ser	Thr	Leu	Tyr	Phe	Ile	Ser	Arg	Gly	Ser	Ile	Glu
625					630					635					640
Ile	Leu	Arg	Asp	Asp	Val	Val	Val	Ala	Ile	Leu	Gly	Lys	Asn	Asp	Ile
			645					650						655	
Phe	Gly	Glu	Pro	Val	Ser	Leu	His	Ala	Gln	Pro	Gly	Lys	Ser	Ser	Ala
		660						665					670		
Asp	Val	Arg	Ala	Leu	Thr	Tyr	Cys	Asp	Leu	His	Lys	Ile	Gln	Arg	Ala
	675						680					685			
Asp	Leu	Leu	Glu	Val	Leu	Asp	Met	Tyr	Pro	Ala	Phe	Ala	Glu	Ser	Phe
	690					695					700				
Trp	Ser	Lys	Leu	Glu	Val	Thr	Phe	Asn	Leu	Arg	Asp	Ala	Ala	Gly	Gly
705					710					715					720
Leu	His	Ser	Ser	Pro	Arg	Gln	Ala	Pro	Gly	Ser	Gln	Asp	His	Gln	Gly
				725					730					735	
Phe	Phe	Leu	Ser	Asp	Asn	Gln	Ser	Gly	Ser	Pro	His	Glu	Leu	Gly	Pro
		740						745					750		
Gln	Phe	Pro	Ser	Lys	Gly	Tyr	Ser	Leu	Leu	Gly	Pro	Gly	Ser	Gln	Asn
		755					760					765			
Ser	Met	Gly	Ala	Gly	Pro	Cys	Ala	Pro	Gly	His	Pro	Asp	Ala	Ala	Pro
	770					775					780				
Pro	Leu	Ser	Ile	Ser	Asp	Ala	Ser	Gly	Leu	Trp	Pro	Glu	Leu	Leu	Gln
785					790					795					800
Glu	Met	Pro	Pro	Arg	His	Ser	Pro	Gln	Ser	Pro	Gln	Glu	Asp	Pro	Asp
				805				810						815	
Cys	Trp	Pro	Leu	Lys	Leu	Gly	Ser	Arg	Leu	Glu	Gln	Leu	Gln	Ala	Gln

Ala	Pro	Arg	Ile	His	Arg	Gly	Thr	Ile	Leu	His	Tyr	Ser	Pro	Phe	Lys			
				245					250					255				
Ala	Val	Trp	Asp	Trp	Leu	Ile	Leu	Leu	Leu	Val	Ile	Tyr	Thr	Ala	Val			
			260					265					270					
Phe	Thr	Pro	Tyr	Ser	Ala	Ala	Phe	Leu	Leu	Ser	Asp	Gln	Asp	Glu	Ser			
		275					280					285						
Gln	Arg	Gly	Thr	Cys	Gly	Tyr	Thr	Cys	Ser	Pro	Leu	Thr	Val	Val	Asp			
	290					295				300								
Leu	Ile	Val	Asp	Ile	Met	Phe	Val	Val	Asp	Ile	Val	Ile	Asn	Phe	Arg			
305					310				315						320			
Thr	Thr	Tyr	Val	Asn	Thr	Asn	Asp	Glu	Val	Val	Ser	His	Pro	Arg	Arg			
				325				330						335				
Ile	Ala	Val	His	Tyr	Phe	Lys	Gly	Trp	Phe	Leu	Ile	Asp	Met	Val	Ala			
			340					345					350					
Ala	Ile	Pro	Phe	Asp	Leu	Leu	Ile	Phe	Arg	Thr	Gly	Ser	Asp	Glu	Thr			
		355					360					365						
Thr	Thr	Leu	Ile	Gly	Leu	Leu	Lys	Thr	Ala	Arg	Leu	Leu	Arg	Leu	Val			
	370					375					380							
Arg	Val	Ala	Arg	Lys	Leu	Asp	Arg	Tyr	Ser	Glu	Tyr	Gly	Ala	Ala	Val			
385					390					395					400			
Leu	Phe	Leu	Leu	Met	Cys	Thr	Phe	Ala	Leu	Ile	Ala	His	Trp	Leu	Ala			
				405					410					415				
Cys	Ile	Trp	Tyr	Ala	Ile	Gly	Asn	Val	Glu	Arg	Pro	Tyr	Leu	Glu	Pro			
		420					425						430					
Lys	Ile	Gly	Trp	Leu	Asp	Ser	Leu	Gly	Ala	Gln	Leu	Gly	Lys	Gln	Tyr			
	435						440					445						
Asn	Gly	Ser	Asp	Pro	Ala	Ser	Gly	Pro	Ser	Val	Gln	Asp	Lys	Tyr	Val			
	450					455				460								
Thr	Ala	Leu	Tyr	Phe	Thr	Phe	Ser	Ser	Leu	Thr	Ser	Val	Gly	Phe	Gly			
465					470					475					480			
Asn	Val	Ser	Pro	Asn	Thr	Asn	Ser	Glu	Lys	Val	Phe	Ser	Ile	Cys	Val			
				485					490					495				
Met	Leu	Ile	Gly	Ser	Leu	Met	Tyr	Ala	Ser	Ile	Phe	Gly	Asn	Val	Ser			
			500					505					510					
Ala	Ile	Ile	Gln	Arg	Leu	Tyr	Ser	Gly	Thr	Ala	Arg	Tyr	His	Thr	Gln			
		515					520					525						
Met	Leu	Arg	Val	Lys	Glu	Phe	Ile	Arg	Phe	His	Gln	Ile	Pro	Asn	Pro			
	530					535					540							
Leu	Arg	Gln	Arg	Leu	Glu	Glu	Tyr	Phe	Gln	His	Ala	Trp	Ser	Tyr	Thr			
545					550					555					560			
Asn	Gly	Ile	Asp	Met	Asn	Ala	Val	Leu	Lys	Gly	Phe	Pro	Glu	Cys	Leu			
			565						570					575				
Gln	Ala	Asp	Ile	Cys	Leu	His	Leu	His	Arg	Ala	Leu	Leu	Gln	His	Cys			
		580						585					590					
Pro	Ala	Phe	Arg	Gly	Ala	Ser	Lys	Gly	Cys	Leu	Arg	Ala	Leu	Ala	Val			
		595					600					605						
Lys	Phe	Lys	Thr	Thr	His	Ala	Pro	Pro	Gly	Asp	Thr	Leu	Val	His	Leu			
	610					615					620							
Gly	Asp	Val	Leu	Ser	Thr	Leu	Tyr	Phe	Ile	Ser	Arg	Gly	Ser	Ile	Glu			
625					630					635					640			
Ile	Leu	Arg	Asp	Asp	Val	Val	Val	Ala	Ile	Leu	Gly	Lys	Asn	Asp	Ile			
			645						650					655				
Phe	Gly	Glu	Pro	Ala	Ser	Leu	His	Ala	Arg	Pro	Gly	Lys	Ser	Ser	Ala			
		660						665					670					
Asp	Val	Arg	Ala	Leu	Thr	Tyr	Cys	Asp	Leu	His	Lys	Ile	His	Arg	Ala			
	675						680					685						
Asp	Leu	Glu	Val	Leu	Asp	Met	Tyr	Pro	Ala	Phe	Ala	Asp	Thr	Phe				
	690				695					700								
Trp	Asn	Lys	Leu	Glu	Val	Thr	Phe	Asn	Leu	Arg	Asp	Ala	Asp	Gly	Gly			
705					710					715					720			
Leu	Gln	Ser	Thr	Pro	Arg	Gln	Ala	Pro	Gly	His	Gln	Asp	Pro	Gln	Gly			

Asp	Ser	Val	Ala	Met	Lys	His	Phe	Lys	Ser	Pro	Thr	Lys	Glu	Ser	Cys
	195						200					205			
Ser	Pro	Ser	Glu	Ala	Asp	Asp	Thr	Lys	Ala	Leu	Ile	Gln	Pro	Ser	Gln
	210					215					220				
Cys	Ser	Pro	Leu	Val	Asn	Ile	Ser	Gly	Pro	Leu	Asp	His	Ser	Ser	Pro
225					230					235					240
Lys	Arg	Gln	Trp	Asp	Arg	Leu	Tyr	Pro	Asp	Met	Leu	Gln	Ser	Ser	Ser
				245					250					255	
Gln	Leu	Thr	His	Ser	Arg	Ser	Arg	Glu	Ser	Leu	Cys	Ser	Ile	Arg	Arg
			260					265					270		
Ala	Ser	Ser	Val	His	Asp	Ile	Glu	Gly	Phe	Asn	Val	His	Pro	Lys	Asn
			275				280					285			
Ile	Phe	Arg	Asp	Arg	His	Ala	Ser	Glu	Asp	Asn	Gly	Arg	Asn	Val	Lys
	290					295					300				
Gly	Pro	Phe	Asn	His	Ile	Lys	Ser	Ser	Leu	Leu	Gly	Ser	Thr	Ser	Asp
305					310					315					320
Ser	Asn	Leu	Asn	Lys	Tyr	Ser	Thr	Ile	Asn	Lys	Ile	Pro	Gln	Leu	Thr
				325					330					335	
Leu	Asn	Phe	Ser	Asp	Val	Lys	Thr	Glu	Lys	Lys	Asn	Thr	Ser	Pro	Pro
			340					345					350		
Ser	Ser	Asp	Lys	Thr	Ile	Ile	Ala	Pro	Lys	Val	Lys	Glu	Arg	Thr	His
			355				360					365			
Asn	Val	Thr	Glu	Lys	Val	Thr	Gln	Val	Leu	Ser	Leu	Gly	Ala	Asp	Val
	370					375					380				
Leu	Pro	Glu	Tyr	Lys	Leu	Gln	Thr	Pro	Arg	Ile	Asn	Lys	Phe	Thr	Ile
385					390					395					400
Leu	His	Tyr	Ser	Pro	Phe	Lys	Ala	Val	Trp	Asp	Trp	Leu	Ile	Leu	Leu
				405					410					415	
Leu	Val	Ile	Tyr	Thr	Ala	Ile	Phe	Thr	Pro	Tyr	Ser	Ala	Ala	Phe	Leu
			420					425					430		
Leu	Asn	Asp	Arg	Glu	Glu	Gln	Lys	Arg	Arg	Glu	Cys	Gly	Tyr	Ser	Cys
			435				440					445			
Ser	Pro	Leu	Asn	Val	Val	Asp	Leu	Ile	Val	Asp	Ile	Met	Phe	Ile	Ile
						455					460				
Asp	Ile	Leu	Ile	Asn	Phe	Arg	Thr	Thr	Tyr	Val	Asn	Gln	Asn	Glu	Glu
465					470					475					480
Val	Val	Ser	Asp	Pro	Ala	Lys	Ile	Ala	Val	His	Tyr	Phe	Lys	Gly	Trp
				485					490					495	
Phe	Leu	Ile	Asp	Met	Val	Ala	Ala	Ile	Pro	Phe	Asp	Leu	Leu	Ile	Phe
			500					505					510		
Gly	Ser	Gly	Ser	Asp	Glu	Thr	Thr	Thr	Leu	Ile	Gly	Leu	Leu	Lys	Thr
			515				520					525			
Ala	Arg	Leu	Leu	Arg	Leu	Val	Arg	Val	Ala	Arg	Lys	Leu	Asp	Arg	Tyr
						535					540				
Ser	Glu	Tyr	Gly	Ala	Ala	Val	Leu	Met	Leu	Leu	Met	Cys	Ile	Phe	Ala
545					550					555					560
Leu	Ile	Ala	His	Trp	Leu	Ala	Cys	Ile	Trp	Tyr	Ala	Ile	Gly	Asn	Val
				565					570					575	
Glu	Arg	Pro	Tyr	Leu	Thr	Asp	Lys	Ile	Gly	Trp	Leu	Asp	Ser	Leu	Gly
			580					585					590		
Thr	Gln	Ile	Gly	Lys	Arg	Tyr	Asn	Asp	Ser	Asp	Ser	Ser	Ser	Gly	Pro
			595				600					605			
Ser	Ile	Lys	Asp	Lys	Tyr	Val	Thr	Ala	Leu	Tyr	Phe	Thr	Phe	Ser	Ser
	610					615					620				
Leu	Thr	Ser	Val	Gly	Phe	Gly	Asn	Val	Ser	Pro	Asn	Thr	Asn	Ser	Glu
625					630					635					640
Lys	Ile	Phe	Ser	Ile	Cys	Val	Met	Leu	Ile	Gly	Ser	Leu	Met	Tyr	Ala
				645					650					655	
Ser	Ile	Phe	Gly	Asn	Val	Ser	Ala	Ile	Ile	Gln	Arg	Leu	Tyr	Ser	Gly
			660					665					670		
Thr	Ala	Arg	Tyr	His	Met	Gln	Met	Leu	Arg	Val	Lys	Glu	Phe	Ile	Arg

Ser Leu Pro Asp Ser Ser Leu Ser Thr Val Gly Ile Leu Gly Leu His
 1170 1175 1180
 Arg His Val Ser Asp Pro Gly Leu Pro Gly Lys
 1185 1190 1195

<210> 57
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PAS domain consensus sequence

<221> VARIANT
 <222> (2)...(2)
 <223> Xaa = Any Amino Acid

<221> VARIANT
 <222> (4)...(4)
 <223> Xaa = Any Amino Acid

<221> VARIANT
 <222> (6)...(9)
 <223> Xaa = Any Amino Acid

<221> VARIANT
 <222> (17)...(17)
 <223> Xaa = Any Amino Acid

<400> 57
 Ile Xaa Tyr Xaa Asn Xaa Xaa Xaa Xaa Glu Leu Thr Gly Leu Ser Arg
 1 5 10 15
 Xaa Glu Val

<210> 58
 <211> 32
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PAC domain consensus sequence

<221> VARIANT
 <222> (4)...(4)
 <223> Xaa = Any Amino Acid

<221> VARIANT
 <222> (6)...(9)
 <223> Xaa = Any Amino Acid

<221> VARIANT
 <222> (12)...(14)
 <223> Xaa = Any Amino Acid

<221> VARIANT
 <222> (16)...(18)
 <223> Xaa = Any Amino Acid

<221> VARIANT
 <222> (22)...(22)
 <223> Xaa = Any Amino Acid

<221> VARIANT
 <222> (24)...(31)
 <223> Xaa = Any Amino Acid

<400> 58
 Arg Lys Asp Xaa Ser Xaa Xaa Xaa Xaa Leu Val Xaa Xaa Xaa Pro Xaa
 1 5 10 15
 Xaa Xaa Glu Asp Gly Xaa Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asp
 20 25 30

<210> 59
 <211> 42
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Cyclic nucleotide gated channel transmembrane
 region domain consensus sequence

<221> VARIANT
 <222> (4)...(4)
 <223> The Xaa at position 4 can be Leu or Ile.

<221> VARIANT
 <222> (5)...(9)
 <223> Xaa = Any Amino Acid

<221> VARIANT
 <222> (15)...(18)
 <223> Xaa = Any Amino Acid

<221> VARIANT
 <222> (23)...(23)
 <223> The Xaa at position 23 can be any amino acid and
 is as few as 3 and as many as 5 amino acid acids.

<221> VARIANT
 <222> (26)...(28)
 <223> Xaa = Any Amino Acid

<221> VARIANT
 <222> (34)...(34)
 <223> Xaa = Any Amino Acid

<221> VARIANT
 <222> (38)...(40)
 <223> Xaa = Any Amino Acid

<400> 59
 Trp Phe Leu Xaa Xaa Xaa Xaa Xaa Xaa Pro Phe Asp Leu Leu Xaa Xaa
 1 5 10 15
 Xaa Xaa Gly Ser Asp Glu Xaa Leu Leu Xaa Xaa Xaa Arg Leu Leu Arg
 20 25 30
 Leu Xaa Arg Val Ala Xaa Xaa Xaa Asp Arg

<210> 60
 <211> 17
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Cyclic nucleotide binding domain (CNBD) consensus
 sequence

 <221> VARIANT
 <222> (1)...(1)
 <223> The Xaa at position 1 can be Leu, Ile, Val, or
 Met.

 <221> VARIANT
 <222> (2)...(2)
 <223> The Xaa at position 2 can be Val, Ile, or Cys.

 <221> VARIANT
 <222> (3)...(4)
 <223> Xaa = Any Amino Acid

 <221> VARIANT
 <222> (6)...(6)
 <223> The Xaa at position 6 can be Asp, Glu, Asn, Gln,
 Thr, or Ala.

 <221> VARIANT
 <222> (7)...(7)
 <223> Xaa = Any Amino Acid

 <221> VARIANT
 <222> (8)...(8)
 <223> The Xaa at position 8 can be Gly, Ala, Cys, or
 Leu.

 <221> VARIANT
 <222> (9)...(10)
 <223> Xaa = Any Amino Acid

 <221> VARIANT
 <222> (11)...(14)
 <223> The Xaa at positions 11 to 14 can be Leu, Ile,
 Val, Met, Phe, or Tyr.

 <221> VARIANT
 <222> (15)...(16)
 <223> Xaa = Any Amino Acid

 <400> 60
 Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5 10 15
 Gly

<210> 61
 <211> 14

<212> PRT
 <213> Artificial Sequence

 <220>
 <223> Cyclic nucleotide binding domain (CNBD) consensus sequence

 <221> VARIANT
 <222> (1)...(1)
 <223> The Xaa at position 1 can be Leu, Ile, Val, Met, or Phe.

 <221> VARIANT
 <222> (4)...(4)
 <223> Xaa = Any Amino Acid

 <221> VARIANT
 <222> (5)...(5)
 <223> The Xaa at position 5 can be Gly, Ala, Ser, or Val.

 <221> VARIANT
 <222> (6)...(6)
 <223> The Xaa at position 6 can be Leu, Ile, Val, Met, or Ser.

 <221> VARIANT
 <222> (7)...(7)
 <223> The Xaa at position 7 can be any amino acid and is as few as 5 and as many as 13 amino acids.

 <221> VARIANT
 <222> (8)...(8)
 <223> The Xaa at position 8 can be Arg or Ser.

 <221> VARIANT
 <222> (9)...(9)
 <223> The Xaa at position 9 can be Ser, Thr, Ala, or Gln.

 <221> VARIANT
 <222> (11)...(11)
 <223> Xaa = Any Amino Acid

 <221> VARIANT
 <222> (12)...(12)
 <223> The Xaa at position 12 can be Leu, Ile, Val, Met, or Ala.

 <221> VARIANT
 <222> (13)...(13)
 <223> Xaa = Any Amino Acid

 <221> VARIANT
 <222> (14)...(14)
 <223> The Xaa at position 14 can be Ser, Thr, Ala, Cys, or Val.

 <400> 61
 Xaa Gly Glu Xaa Xaa Xaa Xaa Xaa Xaa Ala Xaa Xaa Xaa Xaa

1 5 10

<210> 62
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Proline rich domain

<221> VARIANT
<222> (1)...(1)
<223> Xaa = Any Amino Acid

<221> VARIANT
<222> (3)...(4)
<223> Xaa = Any Amino Acid

<221> VARIANT
<222> (6)...(6)
<223> Xaa = Any Amino Acid

<400> 62
Xaa Pro Xaa Xaa Pro Xaa
1 5